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5. Name of your agent *(if you have one)* — MEWBURN ELLIS

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POLYPEPTIDE METHODS AND MEANS

The present invention concerns polypeptide methods and means relating to RAD51, BRCA2 and BRC repeat sequences.

Inheritance of one defective copy of the BRCA2 gene causes increased susceptibility to breast, ovarian and other cancers, with a penetrance approaching 70% by age 70 years [1]. BRCA2 encodes a large protein (3,418 amino acids), which localizes to the nucleus of mitotic cells during S phase of the cell cycle, and is also highly expressed during meiosis. The amino acid sequence of the BRCA2 protein offers few clues to its biological role, because it does not closely resemble other proteins of known function, and has no orthologues in the yeast, fly, or worm genomes.

One remarkable feature of the BRCA2 protein [2] is the presence of eight conserved sequence motifs - the BRC repeats - of about 30 amino acids each, positioned between residues 990 to 2940 in human BRCA2. The high degree of conservation between the BRC repeats in different species is particularly striking when compared to the limited overall sequence similarity among BRCA2 orthologs [3,4], suggesting that the BRC motifs perform an essential function in physiological processes where BRCA2 is implicated. Indeed, the BRC repeats are the primary sites through which BRCA2 binds directly to RAD51 [5-7], a protein with a crucial role in DNA recombination. Like its bacterial homologue RecA, RAD51 coats single-stranded DNA substrates to form a helical nucleoprotein filament, which can invade duplex DNA and pair with homologous nucleotides to initiate the strand exchange reactions that culminate in genetic recombination. When expressed in vitro [5-7], each of the eight BRC repeats in BRCA2 can interact directly with recombinant RAD51. BRC3 and BRC4 encoded in human BRCA2 are particularly efficient at RAD51 binding, whereas BRC5 and BRC6 are not.

There is growing evidence that the interaction between BRCA2 and RAD51 is critical for the biological functions of both molecules [8,9]. Discrete nuclear foci containing RAD51 usually accumulate within the nucleus of mammalian cells exposed to DNA damage. RAD51 foci fail to form in BRCA2-deficient cells [7,10,11], suggesting that BRCA2 transports RAD51 to sites where DNA damage is processed by recombination. Indeed, BRCA2 deficiency leads to a severe defect in the repair of DNA double-strand breaks by recombination [12], and like RAD51 deficiency [13,14], provokes spontaneous instability of chromosome structure during cell division [15,16]. Surprisingly - and in apparent conflict with these data - the activity of RAD51 in nucleoprotein filament formation is suppressed by its interaction with peptides encoding BRC repeats [17]. Collectively, the experimental evidence suggests models in which the intracellular transport of BRCA2-RAD51 complexes and their activity in nucleoprotein filament formation are regulated following DNA damage, perhaps resulting in transitions from 'inactive' to 'active' states [9,17].

A major factor holding back further elucidation of RAD51 and BRCA2 functionality and interaction is the lack of determined crystal structures for these proteins. One reason for this is the difficulty, well known in the art, of forming protein crystals having a quality which is sufficiently high to allow the protein structures to be determined by X-ray crystallography. To date, as far as we are aware, no investigators have been able to identify suitable crystallisation procedures for forming BRCA2/RAD51 complex crystals of the required quality.

An additional difficulty associated specifically with RAD51 is the tendency for RAD51 to aggregate in solution. This tendency has defeated previous attempts to crystallise RAD51.

Disclosure of the Invention

In general aspects, the present invention is concerned with the provision of a RAD51-BRC repeat sequence complex structure and its use e.g. in modelling the interaction of molecular structures such as potential pharmaceutical compounds.

In further general aspects, the present invention is concerned with the provision of mutant RAD51 and BRCA2 polypeptides and preferably a mutant RAD51 polypeptide which has a reduced tendency to aggregate in solution. Such a mutant may be used e.g. in assays for finding compounds which interact with or form part of a RAD51 pathway.

Another general aspect of the present invention concerns a RAD51-BRC repeat sequence chimaera protein. Such a chimaera can be used to form crystals which may be analysed by X-ray crystallography.

These and other aspects and embodiments of the present invention are discussed below.

The above aspects of the invention, both singly and in combination, all contribute to features of the invention which are advantageous.

The present invention is described below in relation to the following figures in which:

Brief Description of the Drawings

Figure 1 sets out Table 1, providing the coordinates of a RAD51-BRCA2 BRC4 complex structure,

Figures 2 sets out Table 2, providing crystallographic data for the complex structure of Table 1,

Figures 3 sets out Table 3, providing a structure-based analysis of BRCA2 BRC sequence conservation,

Figure 4 shows (a) ribbon representations of the RAD51 and BRC4 structures in the RAD51-BRCA2 BRC4 complex, the shorter BRC4 structure being positioned in front of the RAD51 structure and amino- and caboxyl-termini being indicated N and C respectively, and (b) a schematic topology diagram of the complex, the RAD51 secondary structures that are part of the RecA-homology domain being numbered and disordered RAD51 loops L1 and L2 respectively connecting beta strand B4 to alpha helix A5 and B5 to B6 shown as dashed lines (the flexible polypeptide linker connecting the RAD51 to BRC4 being omitted in both (a) and (b)),

Figure 5 shows the interface of the RAD51-BRCA2 BRC4 complex as (a) a solvent-accessible molecular surface generated for the RAD51 interface residues and superimposed with a tube representing the BRC4 interface backbone chain, with stick representations of BRC4 side chains projecting from the BRC4 backbone chain, and (b) a ribbon diagram of the RAD51 interface residues superimposed with a tube representation of the BRC4 interface backbone chain, stick representations of BRC4 side chains projecting from the BRC4 backbone chain, RAD51 side chains projecting from the RAD51 ribbon diagram, and dashed lines representing hydrogen bonds,

Figure 6 shows (a) a close view of the RAD51 ATP-binding pocket, side chains of residues important for ATP binding and hydrolysis, together with adjacent, interacting amino acids, being shown as sticks, the sphere indicating the position of a buried water molecule, and dashed lines representing hydrogen bonds, and (b) a superposition of the phosphate-binding loops of RAD51 and ADP-bound RecA, the atoms of the ADP molecule being drawn as spheres of Van der Waals radii,

Figure 7 shows (a) a superposition of the RAD51-BRCA2 complex on a subunit of the crystallographic RecA filament (omitting RAD51 for clarity), the BRC motif being positioned at the interface between adjacent RecA subunits in the filament, (b) a close view of part of the interface between subunits in the crystallographic RecA filament, the sequence 26-IMRL-29 in the amino terminal tail of RecA mediating polymerisation by antiparallel beta strand pairing, and residues Ile26 and Leu29 representing points of hydrophobic contacts between subunits, (c) a close view of part of the interface between RAD51 and the BRC motif, the BRCA2 sequence 1524-FHTA-1527 interacting with RAD51 via antiparallel beta strand pairing, and residues Phe1524 and Ala1527 contacting RAD51 hydrophobically, and (d) a demonstration of evolutionary conservation of RAD51 residues predicted to be involved in nucleoprotein filament formation, sequences of human DMC1, pyrococcus (an archea bacterium) RADA, bacterial RecA and human BRCA2 with a comparable structural role being aligned underneath, and RAD51 residues completely or highly conserved being boxed, and

Figures 8(a) to (d) shows microscope images obtained from transfected 293T cells. Nuclei in the middle panels of (a), (c) and (d) are stained with the DNA dye ToPro3 (Molecular Probes). In (a) GFP-RAD51 accumulates in nuclear foci. In (b) focus formation is dependent on RAD51 multimerization because co-expression of BRC3/4 (middle panel) prevents GFP-RAD51 focus formation, resulting in its diffuse nuclear distribution. Merged staining in the right hand panel marks cells that co-express GFP-RAD51 with BRC3/4. The cell denoted with a white arrow expresses GFP-RAD51 but not BRC3/4. GFP-RAD51 focus formation occurs in this cell, providing an internal experimental control. In (c) and (d) GFP-tagged mutants of RAD51 do not accumulate in foci.

Detailed Description of the Invention

A. Chimaeras

The present invention provides a RAD51-BRC repeat sequence chimaera protein in which the RAD51 is covalently joined to a BRC repeat sequence. The present invention further provides a nucleic acid encoding the chimaera protein.

Such a protein and such a nucleic acid may be obtained using the methods described in the accompanying examples.

By covalently binding RAD51 to a BRC repeat sequence we have formed a chimaera which for the first time allows RAD51 to be crystallized in a form suitable for X-ray structural analysis.

A flexible polypeptide linker (such as $(Gly)_{12}$, $(Ser)_{12}$, or $(GlySer)_6$) may be used to join the RAD51 and the BRC repeat sequence. Preferably the linker allows substantially unrestrained interaction between the BRC repeat sequence and the RAD51.

The RAD51 is preferably human RAD51. The RAD51 may be a wild-type protein or a variant thereof which is modified, for example by N-terminal truncation so that the truncated RAD51 spans the RecA homology domain. The BRC repeat sequence is preferably a BRCA2 BRC repeat, more preferably a human BRCA2 BRC repeat and even more preferably the human BRCA2 BRC3 or BRC4 repeat.

The same approach may be used to form chimaeras of RAD51 paralogues (such as DMC1, RAD51B, RAD51C, xrcc2, xrcc3, RAD52, RAD54, RAD55 and RAD57) with BRC repeat sequences. The chimaeras should be crystallizable in a form suitable for X-ray structural analysis, even though, insofar as is known, the paralogues themselves have a tendency to agglomerate in solution like RAD51. Thus more general aspects of the present

invention provide (a) a chimaera protein in which a RAD51 paralogue is covalently joined to a BRCA2 BRC repeat and (b) a nucleic acid encoding the chimaera protein.

B. Protein Crystals

In a further aspect, the present invention provides a crystal of a RAD51-BRC repeat sequence complex having the orthorhombic space group $P2_12_12_1$, and unit cell dimensions a = 57.30 Å, b = 59.14 Å, c = 77.20 Å. The crystal contains one complex in the asymmetric unit. Unit cell variability of 5% may be observed in all dimensions. The complex is preferably a RAD51-BRCA2 BRC repeat sequence complex.

Such a crystal may be obtained using the methods described in the accompanying examples. The RAD51 may be N-terminal truncated so that it spans the RecA homology domain. The RAD51-BRC repeat sequence complex may be formed by interaction between the RAD51 and BRC repeat sequence portions of a RAD51-BRC repeat sequence chimaera protein described above.

The methodology used to provide a RAD51-BRC repeat sequence complex crystal illustrated herein may be used generally to provide a RAD51-BRC repeat sequence complex crystal which diffracts X-rays for the determination of atomic coordinates of the complex to a resolution of better than 2.0 Å and preferably better than 1.8 or 1.7 Å.

The invention thus further provides a RAD51-BRC repeat sequence complex crystal which diffracts X-rays for the determination of atomic coordinates of the complex to a resolution of better than 2.0 Å and preferably better than 1.8 or 1.7 Å.

C. Crystal Coordinates

In a further aspect, the present invention also provides a crystal of a RAD51-BRC repeat sequence complex having the three dimensional atomic coordinates of Table 1. An advantageous feature of the structure defined by the atomic coordinates is that it has a high resolution of about 1.7 Å.

Thus for the first time we have been able to provide atomic coordinate data for human RAD51 and a BRC repeat sequence of human BRCA2. More specifically we have provided atomic coordinate data for the interface between RAD51 and the BRC repeat sequence. As shown in relation to the examples, these data reveal the structural basis for the BRCA2-dependent regulation of RAD51 function in DNA recombination, and provide insight into BRCA2 mutations associated with increased susceptibility to cancer.

Table 1 gives atomic coordinate data for a RAD51-BRC repeat sequence complex. In Table 1 the third column denotes the atom; the fourth the residue type; the fifth (where present) the chain identification (A is RAD51, B is BRC repeat sequence, C is an artificial tetrapeptide sequence, and AC1 and AC2 represent alternative side chain conformations for RAD51 amino acids 158, 208, 220, 326 and BRC repeat sequence amino acid 1519); the sixth the residue number (the residue numbering is with respect to the full length wild type protein); the seventh, eighth and ninth columns are the X, Y, Z coordinates respectively of the atom in question in Å; the tenth column the occupancy of the atom; the eleventh the temperature factor of the atom; and the twelfth (where present) the chain identification.

The coordinates of Table 1 provide a measure of atomic location in Å, to 3 decimal places. The coordinates are a relative set of positions that define a shape in three

dimensions, but the skilled person would understand that an entirely different set of coordinates having a different origin and/or axes could define a similar or identical shape. Furthermore, the skilled person would understand that varying the relative atomic positions of the atoms of the structure so that the root mean square deviation of the residue backbone atoms (i.e. the nitrogen-carbon-carbon backbone atoms of the protein amino acid residues) is less than 2.0 Å, preferably less than 1.5 Å, more preferably less than 1.0 Å, even more preferably less than 0.64 Å and most preferably less than 0.5 Å, when superimposed on the coordinates provided in Table 1 for the residue backbone atoms, will generally result in a structure which is substantially the same as the structure of Table 1 in terms of both its structural characteristics and usefulness for RAD51/BRC repeat sequence structure-based analysis. Likewise the skilled person would understand that changing the number and/or positions of the water and ethylene glycol molecules and the magnesium and chloride ions of Table 1 will not generally affect the usefulness of the structure for structure-based analysis.

Thus for the purposes described herein as being aspects of the present invention, it is within the scope of the invention if: the Table 1 coordinates are transposed to a different origin and/or axes; the relative atomic positions of the atoms of the structure are varied so that the root mean square deviation of residue backbone atoms is less than 2.0 Å, preferably less than 1.5 Å, more preferably less than 1.0 Å, even more preferably less than 0.64 Å and most preferably less than 0.5 Å, when superimposed on the coordinates provided in Table 1 for the residue backbone atoms; and/or the number and/or positions of water molecules, ethylene glycol molecules, magnesium ions and/or chloride ions is varied.

Reference herein to the coordinate data of Table 1 thus includes the coordinate data in which one or more individual values of the Table are varied in this way. By "root mean square deviation" we mean the square root of the arithmetic mean of the squares of the deviations from the mean.

Those of skill in the art will appreciate that in many applications of the invention, it is not necessary to utilise all the coordinates of Table 1 but merely a portion of them. For example, as described below, in methods of modelling candidate compounds with RAD51 or BRC repeat sequences, selected coordinates from Table 1 may be used, for example at least 5, preferably at least 10, more preferably at least 50 and even more preferably at least 100 atoms of the RAD51-BRC repeat sequence structure. Likewise, the other applications of the invention described herein, including homology modelling and structure solution, and data storage and computer assisted manipulation of the coordinates, may also utilise all or a portion of the coordinates of Table 1.

D. Mutants

A mutant is a protein characterized by replacement or deletion of at least one amino acid from the wild type protein, or insertion of at least one amino acid into the wild type protein. Such a mutant may be prepared for example by site-specific mutagenesis, or incorporation of natural or unnatural amino acids.

To produce mutants of RAD51 or BRCA2, amino acids present in RAD51 or BRCA2 can be replaced by other amino acids having similar or contrary properties, for example hydrophobicity, hydrophobic moment, antigenicity, propensity to form or break α-helical or β-sheet structures, and so on. Substitutional variants of a protein are those in which at least one amino acid in the protein sequence has been removed and a different

residue inserted in its place. Amino acid substitutions are typically of single residues but may be clustered depending on functional constraints e.g. at a crystal contact. Insertional amino acid variants are those in which one or more amino acids are introduced. This can be amino-terminal and/or carboxy-terminal fusion as well as intrasequence. Examples of amino-terminal and/or carboxy-terminal fusions are affinity tags, MBP tags, and epitope tags.

In some instances, it may be particularly advantageous or convenient to substitute, delete and/or add amino acid residues to a RAD51 or BRCA2 binding pocket or catalytic residue in order to provide convenient cloning sites in cDNA encoding the polypeptide, to aid in purification of the polypeptide, etc. Such substitutions, deletions and/or additions which do not substantially alter the three dimensional structure of RAD51 or the BRCA2 will be apparent to those having skills in the art.

It should be noted that the mutants contemplated herein need not exhibit enzymatic activity. Indeed, amino acid substitutions, additions or deletions that interfere with the activity of RAD51 or BRCA2 but which do not significantly alter the three-dimensional structure of the catalytic region are specifically contemplated by the invention. Such crystalline polypeptides, or the atomic structure co-ordinates obtained there from, can be used to identify compounds that bind to the protein.

One aspect of the present invention provides a mutant RAD51 which has been modified to reduce or eliminate the tendency of RAD51 to spontaneously aggregate into high molecular weight complexes. Thus preferably the mutant RAD51 maintains a monomeric form in solution. The present invention further provides a nucleic acid encoding the mutant RAD51.

The formation of such mutants is described in the accompanying examples. The mutant may be formed by substitution, deletion and/or addition of at least one amino acid in the 85-GFTTATE-91 sequence of human RAD51, or the corresponding sequence in other forms of RAD51.

Such corresponding sequences in other forms of RAD51 are highly conserved and are readily identifiable e.g. by sequence alignment techniques. The sequences for mouse, hamster, fruit fly and yeast are provided in the accompanying examples.

Preferably the mutation substantially alters the functionality of the sequence. For example, in the accompanying examples we replaced the hydrophobic residue Phe86 or Ala89 in the 85-GFTTATE-91 sequence of human RAD51 with hydrophilic glutamic acid. Other suitable mutations would be apparent to the skilled person.

Advantageously, the mutant RAD51 may be crystallised in a form suitable for further X-ray analysis of the RAD51 structure. The mutant RAD51 may also be used in an assay for identifying compounds (e.g. proteins) which interact with or form part of a RAD51 pathway.

E. Homology Modelling

The invention also provides a means for homology modelling of other proteins (referred to below as target proteins). By "homology modelling", it is meant the prediction of related RAD51 or BRC repeat sequence structures based either on X-ray crystallographic data or computer-assisted *de novo* prediction of structure, and involving the manipulation of the coordinate data of Table 1.

Homology modelling as such is a technique that is well known to those skilled in the art (see e.g. Greer, *Science*, Vol. 228, (1985), 1055, and Blundell *et al.*, *Eur. J. Biochem*, Vol.

172, (1988), 513). The techniques described in these references, as well as other homology modelling techniques generally available in the art, may be used in performing the present invention.

Homology modelling extends to target proteins which are analogues or homologues of the RAD51 or BRC repeat sequence whose structures have been determined in the accompanying examples. It also extends to protein mutants of the RAD51 or BRC repeat sequence.

In general, the method involves comparing the amino acid sequences of the RAD51 or BRC repeat of Table 1 with a target protein by aligning the amino acid sequences. Amino acids in the sequences are then compared and groups of amino acids that are homologous (conveniently referred to as "corresponding regions") are grouped together. This method detects conserved regions of the polypeptides and accounts for amino acid insertions or deletions.

Homology between amino acid sequences can be determined using commercially available algorithms. The programs *BLAST*, *gapped BLAST*, *BLASTN*, *PSI-BLAST* and *BLAST 2* sequences (provided by the National Center for Biotechnology Information) are widely used in the art for this purpose, and can align homologous regions of two amino acid sequences. These may be used with default parameters to determine the degree of homology between the amino acid sequence from Table 1 and other target proteins which are to be modelled.

Analogues are defined as proteins with similar three-dimensional structures and/or functions and little evidence of a common ancestor at a sequence level.

Homologues are defined as proteins with evidence of a common ancestor i.e. likely to be the result of evolutionary

divergence and are divided into remote, medium and close sub-divisions based on the degree (usually expressed as a percentage) of sequence identity.

A homologue is defined here as a protein which has at least 15% sequence identity with RAD51 in the RecA homology domain or with a BRC repeat sequence, or one functional domain which is characteristic of RAD51 in the RecA homology domain or of a BRC repeat sequence.

There are two types of homologue: orthologues and paralogues. Orthologues are defined as homologous genes in different organisms, i.e. the genes share a common ancestor coincident with the speciation event that generated them. Paralogues are defined as homologous genes in the same organism derived from a gene/chromosome/genome duplication, i.e. the common ancestor of the genes occurred since the last speciation event.

For the purpose of homology modelling, the present invention also contemplates mutants which are polypeptides obtained (a) by replacing at least one amino acid residue in the native or synthetic RecA homology domain of RAD51 with a different amino acid residue and/or (b) by adding and/or deleting at least one amino acid residue within and/or at the N- and/or C-terminus of the native or synthetic RecA homology domain of RAD51, the polypeptide corresponding to the RecA homology domain of RAD51 and having substantially the same three-dimensional structure as the RecA homology domain of RAD51 from which it is derived.

For the purpose of homology modelling, the present invention further contemplates mutants which are polypeptides obtained (a) by replacing at least one amino acid residue in a native or synthetic BRC repeat sequence with a different amino acid residue and/or (b) by adding and/or deleting at least one amino acid residue within and/or at either or both ends of a native or synthetic BRC repeat sequence, the polypeptide

having one or more sequences corresponding to a BRC repeat sequence and in those sequences having substantially the same three-dimensional structure as the BRC repeat from which they are derived.

By having substantially the same three-dimensional structure is meant having a set of atomic structure co-ordinates that have a root mean square deviation (r.m.s.d.) of less than or equal to about 2.0 Å when superimposed with the atomic structure co-ordinates of the RAD51 from which the mutant is derived when at least about 50% to 100% of the C_α atoms of the RAD51 are included in the superposition.

Once the amino acid sequences of the polypeptides with known and unknown structures are aligned, the structures of the conserved amino acids in a computer representation of the polypeptide with known structure are transferred to the corresponding amino acids of the polypeptide whose structure is unknown. For example, a tyrosine in the amino acid sequence of known structure may be replaced by a phenylalanine, the corresponding homologous amino acid in the amino acid sequence of unknown structure.

The structures of amino acids located in non-conserved regions may be assigned manually by using standard peptide geometries or by molecular simulation techniques, such as molecular dynamics. The final step in the process is accomplished by refining the entire structure using molecular dynamics and/or energy minimization.

Thus the invention provides a method of homology modelling comprising the steps of:

(a) aligning a representation of an amino acid sequence of a target protein of unknown three-dimensional structure with the amino acid sequence of the RAD51 or the BRC repeat sequence of Table 1 to match homologous regions of the amino

acid sequences;

(b) modelling the structure of the matched homologous regions of said target protein of unknown structure on the corresponding regions of the RAD51 or BRC repeat sequence structure as defined by Table 1; and

(c) determining a conformation (e.g. so that favourable interactions are formed within the target protein of unknown structure and/or so that a low energy conformation is formed) for said target protein of unknown structure which substantially preserves the structure of said matched homologous regions.

Preferably one or all of steps (a) to (c) are performed by computer modelling.

In respect of RAD51, the data of Table 1 will be particularly advantageous for homology modelling of proteins such as DMC1, RAD51B, RAD51C, xrcc2, xrcc3, RAD52, RAD54, RAD55 and RAD57. These proteins may be the target protein in the method of the invention described above.

F. Structure Solution

The structure of the RAD51-BRC repeat sequence complex can also be used to solve the crystal structure of other target proteins such as other crystal forms of RAD51, RAD51 mutants, RAD51 homologues, and other complexes of RAD51, and corresponding crystal forms relating to a BRC repeat sequence, where X-ray diffraction data of these target proteins has been generated and requires interpretation in order to provide a structure.

Thus, where X-ray crystallographic or NMR spectroscopic data is provided for a target protein of unknown three-dimensional structure, the structure of the RAD51-BRC repeat sequence complex as defined by Table 1 may be used to interpret that

data to provide a likely structure for the target protein by techniques which are well known in the art, e.g. phasing in the case of X-ray crystallography and assisting peak assignments in NMR spectra.

One method that may be employed for these purposes is molecular replacement. In this method, the unknown crystal structure may be determined using the RAD51 or BRC repeat sequence structure coordinates of this invention as provided herein. This method will provide an accurate structural form for the unknown crystal more quickly and efficiently than attempting to determine such information *ab initio*.

Examples of computer programs known in the art for performing molecular replacement are CNS (Brunger A.T.; Adams P.D.; Rice L.M., Current Opinion in Structural Biology, Volume 8, Issue 5, October 1998, Pages 606-611 (also commercially available from Accelerys San Diego, CA) or AMORE (Navaza, J. (1994). AMoRe: an automated package for molecular replacement. Acta Cryst. A50, 157-163).

Thus, in a further aspect the invention provides a method for determining the structure of a protein, which method comprises;

providing the co-ordinates of Table 1, and

positioning the co-ordinates in the crystal unit cell of said protein so as to provide a structure for said protein.

In a preferred aspect of this invention the RAD51 co-ordinates are used to solve the structure of, for example, DMC1, RAD51B, RAD51C, xrcc2, xrcc3, RAD52, RAD54, RAD55 or RAD57.

The invention may also be used to assign peaks of NMR spectra of such proteins, by manipulation of the data of Table 1.

G. Computer Systems

In another aspect, the present invention provides a system, particularly a computer system, the system containing either:

(a) atomic coordinate data according to Table 1, said data defining the three-dimensional structure of the RAD51-BRC repeat sequence complex or at least selected coordinates thereof;

(b) structure factor data (where a structure factor comprises the amplitude and phase of the diffracted wave) for the RAD51-BRC repeat sequence complex, said structure factor data being derivable from the atomic coordinate data of Table 1;

(c) atomic coordinate data of a target protein generated by homology modelling of the target based on the data of Table 1;

(d) atomic coordinate data of a target protein generated by interpreting X-ray crystallographic data or NMR data by reference to the data of Table 1; or

(e) structure factor data derivable from the atomic coordinate data of (c) or (d).

Such data is useful for a number of purposes, including the generation of structures to analyse the mechanisms of action of RAD51, BRC repeat sequences or related proteins and/or to perform rational drug design of compounds which interact with RA51 or BRC repeat sequences.

As used herein, "a computer system" refers to the hardware means, software means and data storage means used to analyse the atomic coordinate and/or structure factor data of the present invention. The minimum hardware means of the computer-based systems of the present invention typically comprises a central processing unit (CPU), a working memory and data storage means, and e.g. input means, output means etc. Desirably a monitor is provided to visualize structure data.

The data storage means may be RAM or means for accessing a computer readable medium of the invention. Examples of such systems are microcomputer workstations available from Silicon Graphics Incorporated and Sun Microsystems running Unix based, Windows NT or IBM OS/2 operating systems.

In a further aspect, the present invention provides a computer readable storage medium on which is stored thereon either:

(a) atomic coordinate data according to Table 1, said data defining the three-dimensional structure of the RAD51-BRC repeat sequence complex or at least selected coordinates thereof;

(b) structure factor data (where a structure factor comprises the amplitude and phase of the diffracted wave) for the RAD51-BRC repeat sequence complex, said structure factor data being derivable from the atomic coordinate data of Table 1;

(c) atomic coordinate data of a target protein generated by homology modelling of the target based on the data of Table 1;

(d) atomic coordinate data of a target protein generated by interpreting X-ray crystallographic data or NMR data by reference to the data of Table 1; or

(e) structure factor data derivable from the atomic coordinate data of (c) or (d).

As used herein, "computer-readable storage medium" refers to any medium or media which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media such as floppy discs, hard disc storage medium and magnetic tape; optical storage media such as optical discs or CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

By providing such a storage medium, the atomic coordinate data can be routinely accessed to model RAD51, a BRC repeat sequence, or selected coordinates thereof. For example, RASMOL (Sayle et al., *TIBS*, Vol. 20, (1995), 374) is a publicly available computer software package which allows access and analysis of atomic coordinate data for structure determination and/or rational drug design.

On the other hand, structure factor data, which are derivable from atomic coordinate data (see e.g. Blundell et al., in *Protein Crystallography*, Academic Press, New York, London and San Francisco, (1976)), are particularly useful for calculating e.g. difference Fourier electron density maps.

A further aspect of the invention provides a method of providing data for generating structures and/or performing drug design with RAD51/BRC repeat sequences, RAD51/BRC repeat sequence homologues or analogues, complexes of RAD51/BRC repeat sequence with a compound, or complexes of RAD51/BRC repeat sequence homologues or analogues with compounds, the method comprising:

(i) establishing communication with a remote device containing computer-readable data comprising at least one of: (a) atomic coordinate data according to Table 1, said data defining the three-dimensional structure of the RAD51-BRC repeat sequence complex or at least selected coordinates thereof; (b) structure factor data (where a structure factor comprises the amplitude and phase of the diffracted wave) for the RAD51-BRC repeat sequence complex, said structure factor data being derivable from the atomic coordinate data of Table 1; (c) atomic coordinate data of a target protein generated by homology modelling of the target based on the data of Table 1; (d) atomic coordinate data of a target protein generated by interpreting X-ray crystallographic data or NMR data by reference to the data of Table 1; or (e) structure factor data

derivable from the atomic coordinate data of (c) or (d); and

(ii) receiving said computer-readable data from said remote device.

Thus the remote device may comprise e.g. a computer system or a computer-readable storage medium of one of the previous aspects of the invention. The device may be in a different country or jurisdiction from where the computer-readable data is received.

The communication may be via the internet, intranet, e-mail etc. Typically the communication will be electronic in nature, but some or all of the communication pathway may be optical, for example, over optical fibers.

H. Uses of the Structure of the Invention

The crystal structure obtained according to the present invention may be used in several ways for drug design.

We show in the examples below that the BRC repeats encoded in BRCA2 structurally mimic a sequence in RecA that contributes to the interface between successive subunits in the RecA filament, and we present evidence that RAD51 multimerization in nucleoprotein filament formation proceeds through a similar interface. The sequence 85-GFTTATE-91 in RAD51 closely resembles the conserved BRC repeat sequence (GFxTASG) that mimics RecA. Furthermore, replacement of Phe86 or Ala89 in RAD51 with glutamic acid, predicted to disrupt critical hydrophobic contacts, creates mutants that are no longer capable of filament formation when expressed in mammalian cells. Thus, our findings uncover an evolutionarily conserved structural motif that enables RecA and RAD51 to assemble into multimeric filaments essential for DNA recombination, and that has become incorporated into BRCA2, a protein exclusive to higher eukaryotes.

Our work provides a structural rationale for the conservation of residues in different BRC repeats from several different species. Alteration of certain of these residues by cancer-associated mutations is predicted to perturb RAD51 binding, emphasizing the importance of the RAD51-BRC repeat interaction as a target for BRCA2 mutations associated with cancer susceptibility.

BRC repeats are found not only in BRCA2 of vertebrates but also in novel proteins of uncertain function expressed in several parasitic species (such as leishmania and trypanosomes), which our structural analysis suggests will bind and regulate RAD51 orthologues expressed in those species in a manner similar to BRC4. Thus the RAD51-BRC repeat structure may have a role in identifying compounds for treating parasite infection.

Structure-based analysis also identifies several residues in BRC repeats and in RAD51 whose modification by phosphorylation or other means is predicted to affect complex formation, providing a means of linking BRCA2-RAD51 regulation to the pathways that signal DNA damage, blocked replication or cell cycle progression.

Thus our findings provide a structural blueprint that may be useful in structure based drug design. Our work shows that the RAD51-BRCA2 interaction will be particularly vulnerable to small molecule inhibitors because it critically depends on spatially constrained hydrophobic contacts to RAD51 made by three residues (Phe1526, Phe1546 and Ala1527) in BRC4, also conserved in different BRC repeats. Because BRCA2 and RAD51 participate in the repair of DNA breakage [8,9], such inhibitors may prove useful adjuncts to radiation therapy or anti-cancer drugs that induce DNA damage.

Therefore, the determination of the three-dimensional structure of the RAD51-BRC repeat sequence complex provides a basis for the design of new compounds which interact with RAD51 and/or BRC repeat sequences in novel ways.

H.1. Obtaining and Analysing Crystal Complexes

In one approach, the structure of a compound bound to RAD51 or a BRC repeat sequence may be determined by experiment. This will provide a starting point in the analysis of the compound bound to RAD51 or the BRC repeat, thus providing those of skill in the art with a detailed insight as to how that particular compound interacts with RAD51 or a BRC repeat sequence.

Many of the techniques and approaches to structure-based drug design described rely at some stage on X-ray analysis to identify the binding position of a ligand in a ligand-protein complex. A common way of doing this is to perform X-ray crystallography on the complex, produce a difference Fourier electron density map, and associate a particular pattern of electron density with the ligand. However, in order to produce the map (as explained e.g. by Blundell et al., mentioned above) it is necessary to know beforehand the protein 3D structure (or at least the protein structure factors). Therefore, determination of the BRCA2 BRC repeat sequence and RAD51 structures also allows production of difference Fourier electron density maps of RAD51- or BRC repeat sequence-compound complexes and determination of the binding position of a drug, and hence may greatly assist the process of rational drug design.

Accordingly, the invention provides a method for determining the structure of a compound bound to RAD51 or a BRC repeat sequence, said method comprising:

providing a crystal of a complex in which the compound is

bound to RAD51 or a BRC repeat sequence; and

determining the structure of said complex by employing the data of Table 1.

The analysis of such structures may employ (i) X-ray crystallographic diffraction data from the complex and (ii) a three-dimensional structure of RAD51 or the BRC repeat sequence, or at least selected coordinates thereof, to generate a difference Fourier electron density map of the complex, the three-dimensional structure being defined by atomic coordinate data according to Table 1. The difference Fourier electron density map may then be analysed.

Therefore, such complexes can be crystallized and analysed using X-ray diffraction methods, e.g. according to the approach described by Greer et al., *J. of Medicinal Chemistry*, Vol. 37, (1994), 1035-1054, and difference Fourier electron density maps can be calculated based on X-ray diffraction patterns of complexes containing RAD51 or the BRC repeat sequence and the solved structure of RAD51 or the BRC repeat sequence according to Table 1. These maps can then be analysed e.g. to determine whether and where a particular compound binds to RAD51 or the BRC repeat sequence and/or changes the conformation of RAD51 or the BRC repeat sequence.

Electron density maps can be calculated using programs such as those from the CCP4 computing package (Collaborative Computational Project 4. The CCP4 Suite: Programs for Protein Crystallography, *Acta Crystallographica*, D50, (1994), 760-763.). For map visualization and model building programs such as "O" (Jones et al., *Acta Crystallograhica*, A47, (1991), 110-119) can be used.

In addition, in accordance with this invention, RAD51 or BRC repeat sequence mutants may be crystallized in co-complex with known RAD51 or BRC repeat sequence substrates, inhibitors or

novel compounds. The crystal structures of a series of such complexes may then be solved by molecular replacement and compared with that of the structure of Table 1. Potential sites for modification within the various binding sites of the mutant may thus be identified. This information provides an additional tool for determining the most efficient binding interactions, for example, increased hydrophobic interactions, between RAD51 and a chemical entity or compound.

H.2. In Silico Analysis and Design

Although the invention will facilitate the determination of actual crystal structures comprising RAD51 or a BRC repeat sequence and a compound which interacts with RAD51 or the sequence repeat, current computational techniques provide a powerful alternative to the need to generate such crystals and generate and analyse diffraction data. Accordingly, a particularly preferred aspect of the invention relates to *in silico* methods directed to the analysis and development of compounds which interact with the RAD51 structure or the BRC repeat sequence structure of the present invention.

Thus as a result of the determination of the RAD51-BRC repeat sequence complex three-dimensional structure, more purely computational techniques for rational drug design may also be used to design structures whose interaction with RAD51 or the BRC repeat sequence is better understood (for an overview of these techniques see e.g. Walters et al (*Drug Discovery Today*, Vol.3, No.4, (1998), 160-178). For example, automated ligand-receptor docking programs (discussed e.g. by Jones et al. in *Current Opinion in Biotechnology*, Vol.6, (1995), 652-656) which require accurate information on the atomic coordinates of target receptors may be used.

The aspects of the invention described herein which utilize the RAD51 or the BRC repeat sequence structure *in silico* may

be equally applied to both the structure of Table 1 and the models of target proteins obtained by other aspects of the invention. Thus having determined a conformation of a target protein by the method described above, such a conformation may be used in a computer-based method of rational drug design as described herein.

Accordingly, the invention provides a computer-based method for the analysis of the interaction of a molecular structure with a RAD51 or BRC repeat sequence structure of the invention, which comprises:

providing the structure of a RAD51 or BRC repeat sequence of the invention;

providing a molecular structure to be fitted to said RAD51 or BRC repeat sequence structure; and

fitting the molecular structure to the RAD51 or BRC repeat sequence structure.

In an alternative aspect, the method of the invention may utilize the coordinates of atoms of interest of the RAD51 or BRC repeat sequence which are in the vicinity of a putative molecular structure binding region in order to model the pocket in which the structure binds. These coordinates may be used to define a space which is then analysed *in silico*. Thus the invention provides a computer-based method for the analysis of molecular structures which comprises:

providing the coordinates of at least two atoms of a RAD51 or BRC repeat sequence structure of the invention ("selected coordinates");

providing a molecular structure to be fitted to said coordinates; and

fitting the structure to the selected coordinates of the RAD51 or BRC repeat sequence.

In practice, it will be desirable to model a sufficient number of atoms of the RAD51 or BRC repeat sequence as defined by the

coordinates of Table 1 which represent a binding region. Thus, in this embodiment of the invention, there will preferably be provided the coordinates of at least 5, preferably at least 10, more preferably at least 50 and even more preferably at least 100 selected atoms of the RAD51 or BRC repeat sequence structure.

Preferably the selected atoms are atoms which are identified below as contributing to interactions in the RAD51-BRC4 interface or being involved in the RAD51 nucleotide-binding site.

Although different compounds may interact with different parts of the binding region of the RAD51 or BRC repeat sequence, the structure of the RAD51 or BRC repeat sequence allows the identification of a number of particular sites which are likely to be involved in many of the interactions of RAD51 or a BRC repeat sequence with the compound (which may be e.g. a drug candidate). The residues are set out in the accompanying example. Thus in this aspect of the invention, the selected coordinates may comprise coordinates of some or all of these residues.

In order to provide a three-dimensional structure of compounds to be fitted to a RAD51 or BRC repeat sequence structure of the invention, the compound structure may be modeled in three dimensions using commercially available software for this purpose or, if its crystal structure is available, the coordinates of the structure may be used to provide a representation of the compound for fitting to a RAD51 or BRC repeat sequence structure of the invention.

By "fitting", it is meant determining by automatic, or semi-automatic means, interactions between at least one atom of a molecular structure and at least one atom of a RAD51 or BRC repeat sequence structure of the invention, and calculating

the extent to which such an interaction is stable. Interactions include attraction and repulsion, brought about by charge, steric considerations and the like. Various computer-based methods for fitting are described further herein.

More specifically, the interaction of a compound with a RAD51 or BRC repeat sequence can be examined through the use of computer modelling using a docking program such as GRAM, DOCK, or AUTODOCK (see Walters et al., *Drug Discovery Today*, Vol.3, No.4, (1998), 160-178, and Dunbrack et al., *Folding and Design*, 2, (1997), 27-42). This procedure can include computer fitting of compounds to the RAD51 or BRC repeat sequence to ascertain how well the shape and the chemical structure of the compound will bind to the RAD51 or BRC repeat sequence.

Also computer-assisted, manual examination of the binding region structure of RAD51 or a BRC repeat sequence may be performed. The use of programs such as GRID (Goodford, *J. Med. Chem.*, 28, (1985), 849-857) - a program that determines probable interaction sites between molecules with various functional groups and an enzyme surface - may also be used to analyse the active site to predict, for example, the types of modifications which will alter binding interactions with a compound.

Detailed structural information can thus be obtained about the binding of the compound to RAD51 or a BRC repeat sequence, and in the light of this information adjustments can be made to the structure or functionality of the compound, e.g. to alter its interaction with RAD51 or the BRC repeat sequence. The above steps may be repeated and re-repeated as necessary.

Since the BRC repeat sequence is a natural ligand and inhibitor of RAD51, structural and spatial information can be usefully derived from the 3D structure of the RAD51-BRC repeat

sequence complex, to facilitate the identification of a compound that interacts with RAD51 by partially or completely mimicking the mode of interaction found in the complex. A pharmacophore, or more specifically a spatial arrangement of a small group of atoms or a functional group, with a positive contribution to compound affinity toward RAD51, can be derived by an analysis of the geometry of the RAD51-BRC repeat sequence interface. Such a pharmacophore-based approach can be applied in drug discovery. An aspect of the invention thus relates to the use of the RAD51 structure or the BRC repeat sequence structure, or information derived from them, for the design or identification of a compound that mimics the BRC repeat sequence in its mode of interaction with RAD51.

One application is the identification of a compound that satisfies a specified pharmacophore. Accordingly, the invention provides a method for the analysis of molecular structures which comprises:

providing the coordinates of at least two atoms of a RAD51 or BRC repeat sequence structure of the invention;

assigning chemical properties to a spatial arrangement derived from the coordinates; and

providing a molecular structure that satisfies the chemical properties in the specified spatial arrangement.

In one application, the specified pharmacophore can be used for scoring compounds fitted against RAD51, an aim being to select compounds that fulfil the criteria of the pharmacophore, or to screen out, from a number of compounds, those that do not fulfil the criteria. Thus, the method may further comprise:

fitting the structure to the selected coordinates; and

evaluating the fitting based on the extent to which the chemical properties of the specified spatial arrangement are satisfied.

In general, the present invention provides for the use of the structure of a RAD51 or BRC repeat sequence of the invention, or for the use of selected coordinates of the structure, for analysing, designing or screening candidate compounds which (a) share RAD51 or BRC repeat sequence activity, (b) interact with RAD51 or BRC repeat sequence, (c) inhibit RAD51 multimerisation, or (d) inhibit or promote RAD51-BRC binding.

H.3. Compounds of the Invention.

Where the molecular structure of a compound which fits to the RAD51 or the BRC repeat sequence structure of the invention has been identified, the invention further includes the step of obtaining or synthesizing the compound and testing it in an *in vivo* or *in vitro* biological system in order to determine its activity (e.g. its ability to interact with RAD51 or to inhibit RAD51 multimerisation).

For example, compounds that fulfil the criteria of a specified pharmacophore can be assayed for activity against RAD51. Thus the invention may further comprise:

obtaining or synthesizing a compound having a molecular structure which satisfies the pharmacophore, and assaying the compound *in vivo* or *in vitro* in order to determine its activity.

In another aspect, the invention includes a compound which is identified by the methods of the invention described above.

Following identification of such a compound, it may be manufactured and/or used in the preparation, i.e. manufacture or formulation, of a composition such as a medicament, pharmaceutical composition or drug. These may be administered to individuals.

Thus, the present invention extends in various aspects not only to a compound as provided by the invention, but also a

pharmaceutical composition, medicament, drug or other composition comprising such a compound e.g. for treatment (which may include preventative treatment) of disease; a method comprising administration of such a composition to a patient, e.g. for treatment of disease; use of such an inhibitor in the manufacture of a composition for administration, e.g. for treatment of disease; and a method of making a pharmaceutical composition comprising admixing such an inhibitor with a pharmaceutically acceptable excipient, vehicle or carrier, and optionally other ingredients.

The invention is illustrated by the following examples and analysis:

I. Examples and Analysis

I.1. Protein Expression and Purification

In order to favour BRCA2 binding over RAD51 multimerisation, we covalently joined the BRC repeat to RAD51. The BRCA2 BRC type 4 sequence (amino acids 1517 to 1551) was connected to the amino terminus of a RAD51 sequence spanning the RecA homology domain (Ser97 to the natural carboxyl terminus) via the flexible polypeptide linker: $(ThrGlySer)_4MetGly$, designed to allow for unrestrained interaction between the BRC repeat sequence and RAD51. The chimaeric protein was expressed in *E. coli* fused to a double amino-terminal tag consisting of a six histidine sequence followed by a GST tag. The soluble, overexpressed protein was first purified from the crude bacterial lysate by Ni-NTA agarose chromatography. The tag was cleaved by incubation with TEV protease and removed by glutathione agarose chromatography. The protein was purified to homogeneity by two further steps of anion exchange chromatography on a ResourceQ column and gel filtration on a Superdex200 10.30 HR column (Amersham-Pharmacia). The protein

was concentrated to 12 mg/ml (0.36micromolar), flash frozen in liquid nitrogen and stored in aliquots at -80° C.

I.2. Protein Crystallization

Crystals of the RAD51-BRCA2 BRC4 complex were grown in hanging drops by the vapour diffusion method. Drops were prepared by mixing two microliters of protein to two microliters of a 25% ethylene glycol solution, and equilibrated against 750 microliters of the same crystallization solution. Crystals grew at 18°C within a few days to a maximum size of approximately 300×100×100 micrometers. The crystals belong to the space group $P2_12_12_1$ (a = 57.30 Å, b = 59.14 Å, c = 77.20 Å), with one complex in the asymmetric unit.

I.3. Structure Determination and Refinement

The structure of the RAD51-BRC4 complex was determined using phasing information from SIRAS and MAD experiments. An initial screening by native gel electrophoresis [27] identified $KAu(CN)_2$ as a potential heavy atom derivative. X-ray data from a native crystal soaked in 0.5mM $KAu(CN)_2$ for 16 hours were collected to 2 Å resolution. The position of the single gold site was readily determined using direct methods as implemented in Shake 'N' Bake [28]. An initial set of phases was calculated with SHARP [29] and improved by the solvent modification routine available within the program. The resulting set of phases were further refined with ARP/WARP [30], which successfully traced the entire chain of the BRC4 repeat and most of the RAD51 ATPase domain. We also prepared selenomethionine-substituted protein that crystallized under the same conditions as the native material. The selenomethionine-containing crystals were used to collect a two-wavelength MAD dataset (peak and high-energy remote at the Se K edge) at station ID29 of the ESRF in Grenoble (France). The MAD phases proved to be of excellent quality and allowed us to extend the resolution of the

diffraction data to 1.7 Å and considerably improve our model. Crystallographic refinement was performed using the programs REFMAC [31] and CNS [32].

The refined model comprises 1919 protein atoms, 239 water molecules and 4 ethylene glycole molecules. One magnesium ion and one chloride ion were also included in the final model to explain two strong, positive F_o-F_c difference peaks, located at the carboxyl terminus of the short helix in the initial strand-helix-strand motif, and at the amino terminus of helix A1. Crystallographic data for the structure of the human RAD51-BRCA2 BRC4 complex are summarized in Table 2 (shown in Figure 2), the coordinates of the complex structure are provided in Table 1 (shown in Figure 1), and Figure 4 shows (a) ribbon representations of the RAD51 and BRC4 structures and (b) a schematic diagram of the topology of the complex with numbering of the RAD51 secondary structures (the flexible polypeptide linker being omitted in both (a) and (b)).

237 amino acid residues (98.8%) are in the core region of the Ramachandran plot, 3 in the generously allowed region (1.2%) and none in the disallowed region. RAD51 residues 97, 230 to 236 (loop L1 between beta strand B4 and helix H5), 268 to 292 (loop L2 between strands B5 and B6) and BRCA2 BRC4 residues 1517 to 1518 are not visible in the electron density map and are presumably disordered. The linker joining the BRC repeat to RAD51 is also not detectable in the map, with the exception of the initial ThrGlySer triplet. The quality of the map for the RAD51 region between strands B7 and B8 (residues 316 to 321) is poor, indicating that they are partially disordered in the crystals; the conformation of the polypeptide chain for this loop must therefore be considered tentative. Surface area accessibility calculations were carried out in CNS. Figures were prepared with Molscript [33] and Raster3D [34].

I.4. Architecture of the RAD51-BRCA2 BRC4 Complex

The structure of the RAD51-BRCA2 BRC4 complex confirms that RAD51 belongs to the RecA-like family of ATPases (Figure 4), which includes the catalytic subunit of the F1 ATP synthase and the large families of DNA helicases, ABC transporters and the extended AAA-ATPases. RAD51 from Glu98 to its carboxyl terminal residue Asp339 folds into a 3-layer α/β structure with a central, nine-stranded mixed beta sheet (B1 to B9; strand order *987615423*) surrounded by two long, parallel alpha helices (A4 and A5) on one side and three shorter helices (A1 to A3) on the other (Figure 4). The twist angle of the beta sheet increases towards the carboxyl terminus of RAD51, so that the last four antiparallel beta strands can wrap around the amino-terminal strand-loop-strand motif. The ATPase domains of human RAD51 and bacterial RecA [18] are topologically identical and their superposition results in a root mean square deviation of 1.7Å over 160 Cα atoms (out of 210 present in the crystallographic model).

BRC4 remains in continuous contact with the ATPase domain of RAD51 over a sequence stretch of 28 amino acids (Leu1521 to Glu1548), defining a minimal BRC repeat footprint on RAD51 (Figure 4). Residues Phe1524 to Val1532 fold into a beta hairpin with a 3:5 loop (1526-TASGK-1530) structured as a type I turn followed by a beta bulge at residue Gly1529, which has a positive ϕ torsion angle [19]. The hairpin lines up alongside beta strand B3, thereby extending RAD51's beta sheet by two short anti-parallel strands. After the hairpin, the BRC motif wraps around helix A4 of RAD51 by means of a short linker (residues Lys1533 to Ala1535) that kinks abruptly at residue Lys1536 and leads into an amphipathic alpha-helical segment (residues Lys1536 to Val1542). The remaining residues at the carboxyl end of BRC4 (residues Val1542 to Glu1548) form an irregular coil with elements of a 3_{10} helix, that spans helices

A4 and A5 of RAD51, making an angle of 60° to their axes. Altogether, the BRC motif encircles approximately a third of the hypothetical circumference of RAD51 at its point of maximum diameter.

I.5. The RAD51-BRC4 Interface

The RAD51-BRC4 interface is extensive and highly hydrophobic in nature. The total surface area buried during complex formation is 2026 Å^2. Figure 5(a) shows the solvent-accessible molecular surface of the RAD51 interface superimposed with tube and stick representations of the BRC4 interface residues. The BRC motif is decorated throughout its length with hydrophobic residues that keep it in close contact with RAD51. Three main points of contact stand out, involving the residues Phe1524, Ala 1527 and Phe1546.

Table 3 (shown in Figure 3) provides a structure-based analysis of BRCA2 BRC sequence conservation and demonstrates that the residues Phe1524, Ala 1527 and Phe1546 are highly conserved in different BRC repeats. In Table 3 the BRC4 sequence from Leu1521 to Glu1548 is displayed horizontally across the top of the table. Residues within elements of secondary structure are boxed. The twenty different amino acids are shown vertically on the left, grouped according to their chemical nature (hydrophilic at the top, hydrophobic at the bottom, the rest in the middle). Each figure in the table indicates the number of times a certain type of amino acid occurs at a particular position in the BRC repeat. The table contains sequence information relative to a set of 56 BRC repeats from 7 different organisms. The information contained in the table is recapitulated by the BRC consensus sequence reported under it ('*i*' = hydrophobic; '*o*' = hydrophilic; '*a*' = aromatic, '*x*' = no preference).

Phe1524 is located on the strand of the beta hairpin in direct contact with RAD51, and its aromatic ring is completely buried within a hydrophobic cavity formed by the side chains of RAD51 residues Met158, Ile160, Ala190, Ala192, Leu203, Ala207 and Met210. Ala1527, in position L2 of the hairpin loop, places its beta carbon into a small pocket formed by the side chains of RAD51 residues Pro168 Phe166, Leu171, Leu186 and Val189. Phe1546, located in the carboxyl terminal end of the BRC repeat, acts together with Leu1545 to form a wedge embedded between RAD51 helices A4 and A5, and surrounded by residues Leu204, Tyr205, Ser208 (in helix A4) and Met251, Arg254, Leu255, Glu258 and Phe259 (in helix A5). The affinity between BRC4 and RAD51 is further enhanced by hydrophobic contacts involving residues Ile1534 in the linker region, and the hydrogen-bonded Ser1538, Leu1539 and Val1542 in the alpha helix.

Although not as numerous as the hydrophobic interactions, contacts of a polar and charged nature also take place (see Figure 5(b)). The beta hairpin keeps BRC4 in register relative to RAD51 through a set of three continuous, antiparallel main chain-to-main chain hydrogen bonds linking the BRC4 sequence 1525-HTA-1527 to the 190-AYA-192 sequence in strand B3 of RAD51. Asp187 of RAD51 accepts a hydrogen bond from Ser1528, in position L3 of the BRC4 hairpin loop, and interacts electrostatically with Lys1530. Moreover, Glu213 of RAD51 accepts a hydrogen bond from Ser1538 of BRC4, in what is likely to represent a particularly significant contact, because the two side chains are poised for interaction. The position of the Ser1538 side chain is determined by a stacking interaction with BRC4 Ala1535 and RAD51 Val212, while Glu213 is hydrogen bonded to the main chain nitrogen of Ala1535 and, via a water molecule, to the main chain carbonyl of Lys1533. Finally, Glu1548, at the carboxyl end of the BRC4 motif, forms an ion pair with Arg250 of RAD51.

Additional interactions involving residues that are not strongly conserved across BRC repeats help to explain the higher affinity [7] of the type 4 repeat towards RAD51 relative to other repeat types. For instance, the tandem repeat of leucine residues 1521 and 1522 are in hydrophobic contact with the side chains of RAD51 residues Phe195 and His199, and the main chain carbonyl of Leu1522 accepts a hydrogen bond from the His199 side chain. His1525 forms a pseudo-hydrophobic core by packing against the aliphatic portions of Lys1535 and Thr1520 side chains and is also hydrogen bonded to the main chain carbonyl of Thr1520, thus conferring further stability to the beta hairpin conformation.

I.6. A Structure-Based Analysis of BRCA2 BRC Sequence Conservation

The structure of the RAD51-BRC4 complex permits the rationalization of the pattern of sequence conservation displayed by BRC repeats across different repeat types and organisms (Table 3). The most amino-terminal residue to be significantly conserved, Gly1523, is found at a point of secondary structure transition, in a spatially constrained environment at the protein-protein interface. Glycine or serine account for 60% of occurrences at this position, with other less frequent residues being generally of a hydrophobic nature.

Residues 1524-FHTASGK-1530, with the exception of His1525, form a contiguous block of highly conserved amino acids. Phe1524 is the single most conserved BRC residue (present in 89% of the sequences in a set of 56 BRC repeats from seven different organisms): the structure shows that it is involved in a crucial recognition interaction with RAD51. Thr1526 does not contact RAD51, but accepts a hydrogen bond from the main chain nitrogen of Lys1530 that is essential for the conformation of the 3:5 hairpin loop. Thr1526 also donates a

hydrogen bond to the hydroxyl function of Ser1528, thus keeping it poised for interaction with RAD51 Asp187. The amino acids threonine or serine account for 93% of occurrences at this position. Like Phe1524, Ala1527 (conserved in 82% of BRC repeats) provides another important point of hydrophobic contact with RAD51. Ser1528 (59%) and Lys1530 (79% preference for a basic residue) are engaged in a polar interaction with Asp187 of RAD51. The preference for a glycine, serine or asparagine (combined frequency of 93%) at position 1529 is dictated by the conformational requirement for a residue that can tolerate a positive ϕ torsion angle.

Two positions in the linker connecting the beta hairpin to the alpha helix (Val1532 and Ile1534 in BRC4) show a strong preference for aliphatic, branched amino acids (80% and 93% respectively for isoleucine, leucine or valine). The structure demonstrates that Val1532 and Ile1534 contribute to the continuous adherence of the BRC4 motif to the RAD51 surface, through an hydrophobic contact with Met210 of RAD51. Position 1535 marks a point of conformational transition to an alpha helical region, and a serine is found to be prevalent here (with 70% occurrence), likely because of its propensity to cap the helix at its amino terminus.

Within the amphipathic helix, conserved residues including Ser1538 (50% preference) and Leu1539 (89% combined preference for Leu, Ile or Val) make hydrophobic and hydrogen bonded interactions with RAD51. BRC position 1542 shows a clear preference for Val, Ala or Ser (79% combined frequency), explained by the structure, where Val1542 marks a point of close contact between BRC4 and helix A4 of RAD51, defining the preference for a small amino acid capable of hydrophobic interaction. However, the strong preference for Lys at positions 1541 (79%) and 1543 (68% combined with arginine) is perplexing because these residues are solvent exposed and do

not contact RAD51. Interestingly, Arg rarely occupies position 1541, consistent with a specific role for lysine, and suggesting that sequence conservation within BRC sequences is not only dictated by their interaction with RAD51.

Leu1545 and Phe1546 in BRC4 are involved in extensive hydrophobic interactions with residues on helices A4 and A5 of RAD51. Indeed, hydrophobic residues are strongly represented at these positions in different BRC repeats (89% and 93% conservation respectively). The structure further demonstrates that, whereas BRC4 residue 1545 is partially solvent exposed, and can therefore accommodate a number of different side chains, the spatial restraints on residue 1546 are much tighter, as its side chain penetrates deeper into the RAD51-BRC interface. In agreement with our observation, position 1545 shows only a general hydrophobic preference, whereas position 1546 requires either a phenylalanine or a leucine. The most carboxyl terminal position to show a distinct sequence preference is 1548, which selects for an acidic residue (80% combined conservation for aspartic and glutamic acid). In the crystal structure, Glu1548 forms a salt link with Arg250 of RAD51.

Our analysis shows that the BRC motif is reminiscent of a Velcro strip in the way it adheres to RAD51, that is, through a large number of contacts that are relatively independent from one another. This observation suggests that BRC repeats that differ widely from the consensus, may still retain the capacity to bind RAD51. The elimination of one or a few contact points would weaken the overall binding affinity, without abolishing binding altogether. The BRC sequence might therefore have arisen as a molecular frame suitable for the evolution of amino acid sequences with a wide range of affinities to RAD51, with potential implications for the regulation of RAD51 function by BRCA2.

I.7. The Human RAD51 Nucleotide-Binding Site

The structure of BRCA2-bound RAD51 reveals some unexpected features of its nucleotide-binding site (see Figures 6(a) and (b)). Lys133 and Thr134, in Walker motif A (127-GEFRTGKT-134), and Asp222, in Walker motif B (218-LLIVD-222), are sequestered in a solvent-inaccessible hydrogen-bonding network that extends to Tyr159, Asp161 and Thr165 via a buried water molecule (Figure 6(a)). Exposed Phe129 at the tip of the phosphate-binding loop (P-loop or Walker motif A) buries part of its aromatic ring in a hydrophobic interaction with Thr134 and Thr165. These contacts do not take place in RecA [18,20], because Lys72 and Thr73 of motif A are further apart from Asp144 in motif B, whereas Glu68 replaces Phe129 in the P-loop. Possibly reflecting the presence of this additional set of interactions, the overall conformation of the P-loop is different in RAD51. A 3-D superposition (Figure 6(b)) shows that, whereas the P-loop remains unchanged in the apo- and ADP-bound forms of RecA [18,20], in BRCA2-bound RAD51 it adopts a more closed conformation that is unlikely to be compatible with its occupation by the ATP phosphates. Although the BRC repeat does not directly mask the ATP-binding site, we speculate that it may cause an indirect conformational effect when bound to RAD51 that inhibits ATP binding.

I.8. Regulation of RAD51 Nucleoprotein Filament Formation by BRCA2

RAD51 forms helical nucleoprotein filaments on DNA substrates that catalyse pairing and strand exchange between homologous DNA molecules, an essential step in homologous recombination [21,22]. Biological data show that filament formation is abolished when RAD51 is bound to BRC repeat peptides. *In vivo*, over-expression of BRC repeats suppresses the accumulation of RAD51 into nuclear foci after exposure of cells to DNA

damaging agents [7]. *In vitro*, incubation of RAD51 with BRC repeat peptides removes its ability to form nucleoprotein filaments on DNA substrates [17]. Finally, the tendency of RAD51 to spontaneously aggregate into high molecular weight complexes, even in the absence of DNA, is prevented by interaction with BRC repeats, which maintains RAD51 in a monomeric form [17].

The structural basis for filament formation by RAD51 is not known [23,24]. In order to gain an insight into the mechanism deployed by BRCA2 to regulate RAD51 filament formation, we analysed the RAD51-BRCA2 interaction in the context of the crystallographic RecA filament (see Figures 7(a) to (d)). In the crystal [18], the RecA molecules pack into a spiral that resembles the nucleoprotein filament formed *in vivo*. Overlaying the RAD51-BRCA2 complex on RecA results in the localization of the BRC beta hairpin at the interface between two adjacent RecA molecules [18] within the crystallographic filament (Figure 7(a)). Surprisingly, BRC4 residues 1523-GFHTASG-1529 superimpose closely onto the RecA sequence 25-SIMRLGE-31, which is part of the interface between RecA subunits. RecA residues 27-MRL-29 add in fact an anti-parallel beta strand to the central beta sheet of a neighbouring RecA molecule, in an identical fashion to the interaction of BRC4 residues 1525-HTA-1527 with RAD51 in the RAD51-BRCA2 complex (see Figures 7(b) and (c)). Moreover, RecA residues Ile26 and Leu29 make comparable hydrophobic contacts to those made by Phe1524 and Ala1527 of BRC4 with RAD51.

The superposition analysis provides a strong clue concerning the mechanism adopted by BRCA2 to regulate RAD51 function - BRCA2 binding prevents formation of the nucleoprotein filament by interfering with a crucial contact between RAD51 subunits, and the specific role of the BRC repeats is to mimic the conformation of the RAD51 segment involved in such contact.

One prediction of our proposed mechanism is that sequence similarity should be found between the BRC motif and the region of the RAD51 sequence with a putative role in multimerization analogous to that performed by RecA sequence 25-SIMRLGE-31. Indeed, careful inspection of the RAD51 sequence for short motifs resembling the BRC consensus GFxTASG motif identifies the highly conserved sequence 85-GFTTATE-91 in the RAD51 linker between the amino terminal domain and the catalytic core (Figure 7(d)).

To test the proposed mechanism, we constructed mutant RAD51 molecules in which amino acids Phe86 and Ala89 within the sequence 85-GFTTATE-91 were replaced by glutamic acid.

I.9. Formation and Analysis of RAD51 Mutants

Mutant RAD51 molecules (Phe86Glu or Ala89Glu) were fused at their amino terminus to the green fluorescent protein (GFP) reporter before transfection into human cell lines. This was accomplished for each of the Phe86Glu and Ala89Glu mutations by using the QuickChange system (Stratagene) to perform site-directed mutagenesis into a cDNA construct encoding the wild-type RAD51-GFP fusionin pEGFP-C1 (Clontech).

Furthermore, the sequence encoding BRC3 and BRC4 from human BRCA2 was fused at its C-terminus to three consensus nuclear localization signals in the vector pEF-Myc-Nuc (Clontech).

Constructs were verified by nucleotide sequencing. Experiments were carried out 72-96 hrs after transfection of plasmids into 293T cells using the calcium phosphate method. Microscopic images were obtained using a Zeiss LSM510 confocal system equipped with ZeissVision software.

Each of the Phe86Glu and Ala89Glu mutations is predicted to eliminate a critical hydrophobic contact at the RAD51 subunit

interface and therefore abolish or significantly weaken RAD51's ability to form filaments.

GFP-RAD51 wild-type, GFP-RAD51 F86E and GFP-RAD51 A89E are expressed at equivalent levels after transfection. As previously observed for endogenous RAD51 [25,26], GFP-RAD51 wild-type accumulates in discrete nuclear foci that represent presumptive sites of DNA damage processing in dividing cells (Figure 8(a)). Formation of these foci is dependent upon RAD51 multimerization, because it is not detected when peptides encoding BRC3 and BRC4 are co-expressed in the same cells (Figure 8(b)); a diffuse nuclear localization of wild-type RAD51 is observed instead, reminiscent of the distribution of GFP alone. Strikingly we find that, when expressed in cells, GFP-RAD51 F86E (Figure 8(c)) and GFP-RAD51 A89E (Figure 8(d)) fail to form foci and are distributed diffusely throughout the nucleus, thus confirming our prediction of an essential role for Phe86 and Ala89 in RAD51 filament formation.

Based on our crystallographic and biological data we therefore conclude that the RAD51 sequence 85-GFTTATE-91 forms an essential part of the interface between RAD51 monomers in the nucleoprotein filament, and residues Phe86 and Ala98 constitute essential points of hydrophobic contact. The sequences 85-GFTTATE-91 in RAD51 and 25-SIMRLGE-31 in RecA mediate a mode of association between subunits that represent a common structural feature of their nucleoprotein filaments.

We further conclude that BRCA2 blocks nucleoprotein filament formation by binding to RAD51 with the BRC consensus sequence GFxTASG, which structurally mimics the RAD51 sequence 85-GFTTATE-91. In the RAD51-BRC4 complex, BRC4 residues Phe1524 and Ala1527 play the same roles that RAD51 residues Phe86 and Ala89 have in the association between RAD51 monomers. The interaction surface between RAD51 and the BRC repeat is more

extensive than that provided by the GFxTASG sequence only, as would be expected for a dominant antagonist interaction.

I.10. Structure-Based Analysis of Cancer-Associated Mutations

Point mutations affecting conserved residues within the BRC repeats predicted to be important for RAD51 binding occur in patients who develop familial breast cancer (Breast Cancer Information Core database, accessible at http:// www.nhgri.nih.gov/Intramural_research/Lab_transfer/Bic/). The common cancer-associated Thr1526 -> Ala mutation impairs the ability of a BRCA4 peptide to bind RAD51 [7,17]. The structure shows that formation of a hydrogen bond between the hydroxyl function of Thr1526 and the main chain nitrogen of Lys1530 is critical to the conformational integrity of the BRC hairpin loop (Figure 5b). The mutation therefore impairs the affinity of BRCA2 to RAD51 by destabilizing the conformation of the beta hairpin that apposes the BRC repeat to the surface of RAD51. Consistent with the notion that the hydroxyl function mediates an essential interaction, position 1526 is occupied by either a threonine or a serine in 52 out of 56 BRC repeat sequences from seven different organisms (Table 3). BRC repeats in which the threonine is replaced are unlikely to assume the 3:5 hairpin loop conformation required for efficient binding to RAD51. Loss of the critical hydroxyl function at a position analogous to that occupied by Thr1526 in BRC4 has been noted in breast cancer-associated mutations that affect BRC1 (Thr1012 -> Arg) or BRC7 (Thr1981 -> Ile).

Another point mutation associated with familial breast cancer changes Gly1529 in BRC4, at the fourth position of the 3:5 hairpin loop, to arginine. Conformational restraints on position 1529 lead to selection of amino acids able to adopt a positive ϕ torsion angle, and glycine, serine or asparagine are indeed found in 52 of 56 BRC sequences (Table 2).

Replacement of glycine by arginine will disrupt the conformation of the BRC beta hairpin and lead thereby to loss of RAD51 binding capacity.

Thus, structure-based analysis of cancer-associated point mutations affecting the BRC repeats suggests that inheritance of a single alteration that impairs RAD51 binding capacity in just one repeat is enough to cause increased breast cancer susceptibility. One explanation for why the remaining seven BRC repeats should not suffice to preserve function is that the eight BRC repeats present in all vertebrate species work together as a RAD51-binding module whose overall topology is critical for function. For instance, the spacing between individual BRC repeats observed in vertebrate species as evolutionarily distant as chickens and humans is highly conserved. This hints at the possibility [9] that interactions with successive BRC repeats in BRCA2 may help to order the distribution of RAD51 molecules in space when, for example, they are being loaded onto substrate DNA during nucleoprotein filament formation, or during removal from established filaments. Alterations that diminish the RAD51 binding capacity of just one of the eight BRC repeats could perturb such functions by interfering with spatial relationships between RAD51 molecules bound to BRCA2.

It has also been suggested that regulation of RAD51 function by BRCA2 may also be modulated by physiological modifications such as phosphorylation [9,17]. For instance, phosphorylation of Thr1526 in BRC4 would be predicted to decrease RAD51 binding affinity by destabilising the BRC repeat conformation, whereas phosphorylation of Ser1528 or Ser1538 would disrupt polar contacts with Asp187 or Glu213, respectively, in RAD51. The strong conservation of lysine residues at positions 1541 and 1543 in the helical region of BRC4, which do not make contacts with RAD51, raises the possibility that their solvent exposed

amino groups could serve as a target for covalent modifications. From this perspective, we speculate that cancer-associated changes that replace lysine residues corresponding to these conserved positions in BRC1 (Lys1026 ->Glu or Asn) and BRC5 (Lys1691->Asn) may interfere with such events.

Other point mutations in BRCA2 associated with cancer predisposition, such as the frequent change D1420Y near BRC3, fall outside the boundaries of the BRC repeat whose structure we have determined here. An extended BRC3 peptide, which spans the Asp1420 residue, efficiently inhibits nucleoprotein filament formation by RAD51, a property that is abolished in the D1420Y mutant [17]. BRCA2 residues outside the BRC consensus sequence defined in this work can therefore additionally contribute to the BRC-RAD51 interaction.

Given that changes in BRCA2 which perturb RAD51 binding give rise to cancer predisposition, our findings raise the possibility that mutations or polymorphisms in RAD51 that impair its interaction with BRCA2 may work in a similar fashion. One reason why such alterations may not yet have been described in breast (or other) cancers is that only a limited number of cases has so far been analysed. Further studies that focus on the prevalence of RAD51 alterations in breast cancers with a familial pattern of incidence may therefore be warranted.

While the invention has been described in conjunction with the exemplary embodiments described above, many equivalent modifications and variations will be apparent to those skilled in the art when given this disclosure. Accordingly, the exemplary embodiments of the invention set forth are considered to be illustrative and not limiting. Various changes to the described embodiments may be made without departing from the spirit and scope of the invention.

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These references, and the other references mentioned above, are hereby incorporated by reference.

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Claims

1. A crystal of a RAD51-BRC repeat sequence complex.

2. A crystal according to claim 1 having the orthorhombic space group $P2_12_12_1$, and unit cell dimensions a = 57.30 Å ± 5%, b = 59.14 Å ± 5%, c = 77.20 Å ± 5%.

3. A crystal according to claim 1 which diffracts X-rays for the determination of atomic coordinates of the complex to a resolution of better than 2.0 Å.

4. A crystal according to claim 1 having the three dimensional atomic coordinates of Table 1.

5. A RAD51-BRC repeat sequence chimaera protein in which the RAD51 is covalently joined to the BRC repeat sequence.

6. A RAD51 paralogue-BRC repeat sequence chimaera protein in which the RAD51 paralogue is covalently joined to the BRC repeat sequence.

7. A nucleic acid encoding the chimaera protein of claim 5 or 6.

8. A mutant RAD51 which has been modified to reduce or eliminate the tendency of RAD51 to spontaneously aggregate into high molecular weight complexes.

9. A mutant RAD51 which has been modified by substitution, deletion and/or addition of at least one amino acid in the 85-GFTTATE-91 sequence of human RAD51, or the corresponding sequence in other forms of RAD51.

10. A nucleic acid encoding the mutant RAD51 of claim 8 or 9.

11. A method of homology modelling comprising the steps of:

(a) aligning a representation of an amino acid sequence of a target protein of unknown three-dimensional structure

with the amino acid sequence of the RAD51 or the BRC repeat sequence of Table 1 to match homologous regions of the amino acid sequences;

(b) modelling the structure of the matched homologous regions of said target protein of unknown structure on the corresponding regions of the RAD51 or BRC repeat sequence structure as defined by Table 1; and

(c) determining a conformation for said target protein of unknown structure which substantially preserves the structure of said matched homologous regions.

12. A method for determining the structure of a protein, which method comprises;

providing the co-ordinates of Table 1, and

positioning the co-ordinates in the crystal unit cell of said protein so as to provide a structure for said protein.

13. A method for determining the structure of a compound bound to RAD51 or a BRC repeat sequence, said method comprising:

providing a crystal of a complex in which a compound is bound to RAD51 or a BRC repeat sequence; and

determining the structure of said complex by employing the data of Table 1.

14. A computer-based method for the analysis of the interaction of a molecular structure with RAD51 or BRC repeat sequence, which comprises:

providing the structure of RAD51 or a BRC repeat sequence as defined by Table 1;

providing a molecular structure to be fitted to said RAD51 or BRC repeat sequence structure; and

fitting the molecular structure to the RAD51 or BRC repeat sequence structure.

15. A computer-based method for the analysis of the interaction of a molecular structure with RAD51 or BRC repeat sequence, which comprises:

providing the coordinates of at least two atoms of RAD51 or a BRC repeat sequence structure as defined by Table 1;

providing a molecular structure to be fitted to said coordinates; and

fitting the structure to the said coordinates.

16. A method of determining the biological activity of a compound, which comprises:

identifying a compound which fits to RAD51 or a BRC repeat sequence by performing the method of claim 14 or 15;

obtaining or synthesizing the compound; and

testing the compound in an *in vivo* or *in vitro* biological system in order to determine the activity of the compound.

17. A compound which is identified by the method of claim 14 or 15.

FIGURE 1

Table 1 Coordinate data on the BRC4-RAD51 complex.

ATOM	1	CB	GLU	A	98	54.122	26.467	6.057	1.00	41.21	A
ATOM	2	CG	GLU	A	98	55.636	26.317	6.015	1.00	45.64	A
ATOM	3	CD	GLU	A	98	56.085	25.256	5.027	1.00	47.43	A
ATOM	4	OE1	GLU	A	98	55.620	24.103	5.147	1.00	49.28	A
ATOM	5	OE2	GLU	A	98	56.901	25.572	4.134	1.00	49.29	A
ATOM	6	C	GLU	A	98	51.999	26.666	4.744	1.00	34.53	A
ATOM	7	O	GLU	A	98	51.235	27.538	5.157	1.00	34.61	A
ATOM	8	N	GLU	A	98	53.866	28.288	4.399	1.00	38.15	A
ATOM	9	CA	GLU	A	98	53.509	26.878	4.717	1.00	37.21	A
ATOM	10	N	ILE	A	99	51.587	25.484	4.306	1.00	30.62	A
ATOM	11	CA	ILE	A	99	50.181	25.125	4.226	1.00	26.62	A
ATOM	12	CB	ILE	A	99	49.982	24.054	3.143	1.00	28.34	A
ATOM	13	CG2	ILE	A	99	48.540	23.603	3.115	1.00	29.76	A
ATOM	14	CG1	ILE	A	99	50.421	24.613	1.790	1.00	29.12	A
ATOM	15	CD1	ILE	A	99	50.399	23.600	.678	1.00	33.00	A
ATOM	16	C	ILE	A	99	49.542	24.625	5.516	1.00	22.96	A
ATOM	17	O	ILE	A	99	50.152	23.893	6.292	1.00	22.20	A
ATOM	18	N	ILE	A	100	48.299	25.039	5.728	1.00	19.56	A
ATOM	19	CA	ILE	A	100	47.524	24.619	6.885	1.00	16.84	A
ATOM	20	CB	ILE	A	100	46.967	25.825	7.679	1.00	16.90	A
ATOM	21	CG2	ILE	A	100	45.957	25.344	8.714	1.00	18.72	A
ATOM	22	CG1	ILE	A	100	48.113	26.580	8.358	1.00	19.95	A
ATOM	23	CD1	ILE	A	100	47.669	27.845	9.089	1.00	22.55	A
ATOM	24	C	ILE	A	100	46.356	23.824	6.315	1.00	15.59	A
ATOM	25	O	ILE	A	100	45.805	24.185	5.275	1.00	14.24	A
ATOM	26	N	GLN	A	101	45.999	22.731	6.978	1.00	13.53	A
ATOM	27	CA	GLN	A	101	44.887	21.907	6.523	1.00	15.11	A
ATOM	28	CB	GLN	A	101	45.348	20.464	6.330	1.00	19.35	A
ATOM	29	CG	GLN	A	101	46.592	20.374	5.458	1.00	26.50	A
ATOM	30	CD	GLN	A	101	46.427	19.451	4.273	1.00	31.87	A
ATOM	31	OE1	GLN	A	101	45.487	19.588	3.488	1.00	35.05	A
ATOM	32	NE2	GLN	A	101	47.350	18.507	4.129	1.00	33.92	A
ATOM	33	C	GLN	A	101	43.786	21.993	7.564	1.00	13.47	A
ATOM	34	O	GLN	A	101	43.959	21.568	8.706	1.00	15.75	A
ATOM	35	N	ILE	A	102	42.654	22.557	7.161	1.00	10.05	A
ATOM	36	CA	ILE	A	102	41.520	22.748	8.060	1.00	8.05	A
ATOM	37	CB	ILE	A	102	40.706	23.983	7.633	1.00	8.89	A
ATOM	38	CG2	ILE	A	102	39.544	24.206	8.599	1.00	8.83	A
ATOM	39	CG1	ILE	A	102	41.620	25.215	7.602	1.00	11.08	A
ATOM	40	CD1	ILE	A	102	41.023	26.415	6.880	1.00	9.86	A
ATOM	41	C	ILE	A	102	40.604	21.531	8.085	1.00	8.43	A
ATOM	42	O	ILE	A	102	40.166	21.054	7.042	1.00	8.83	A
ATOM	43	N	THR	A	103	40.309	21.036	9.282	1.00	8.44	A
ATOM	44	CA	THR	A	103	39.446	19.868	9.411	1.00	9.31	A
ATOM	45	CB	THR	A	103	39.386	19.368	10.872	1.00	10.02	A
ATOM	46	OG1	THR	A	103	38.605	18.164	10.929	1.00	11.79	A
ATOM	47	CG2	THR	A	103	38.755	20.417	11.776	1.00	11.70	A
ATOM	48	C	THR	A	103	38.020	20.116	8.923	1.00	9.93	A
ATOM	49	O	THR	A	103	37.449	21.186	9.141	1.00	8.54	A
ATOM	50	N	THR	A	104	37.456	19.110	8.259	1.00	10.38	A
ATOM	51	CA	THR	A	104	36.091	19.174	7.737	1.00	11.01	A
ATOM	52	CB	THR	A	104	35.912	18.256	6.510	1.00	11.26	A
ATOM	53	OG1	THR	A	104	36.128	16.896	6.914	1.00	14.11	A
ATOM	54	CG2	THR	A	104	36.892	18.613	5.415	1.00	12.62	A
ATOM	55	C	THR	A	104	35.090	18.688	8.784	1.00	11.39	A
ATOM	56	O	THR	A	104	33.878	18.830	8.604	1.00	12.53	A
ATOM	57	N	GLY	A	105	35.598	18.109	9.868	1.00	10.65	A
ATOM	58	CA	GLY	A	105	34.724	17.582	10.901	1.00	11.97	A
ATOM	59	C	GLY	A	105	34.619	16.071	10.780	1.00	13.09	A
ATOM	60	O	GLY	A	105	34.156	15.390	11.699	1.00	13.32	A
ATOM	61	N	SER	A	106	35.052	15.550	9.634	1.00	12.40	A
ATOM	62	CA	SER	A	106	35.033	14.115	9.363	1.00	14.20	A
ATOM	63	CB	SER	A	106	34.242	13.835	8.079	1.00	14.61	A

ATOM	64	OG	SER	A	106	34.505	12.528	7.589	1.00	14.19	A
ATOM	65	C	SER	A	106	36.453	13.563	9.217	1.00	14.25	A
ATOM	66	O	SER	A	106	37.230	14.041	8.391	1.00	13.00	A
ATOM	67	N	LYS	A	107	36.788	12.553	10.017	1.00	15.63	A
ATOM	68	CA	LYS	A	107	38.117	11.946	9.951	1.00	17.24	A
ATOM	69	CB	LYS	A	107	38.279	10.867	11.026	1.00	21.76	A
ATOM	70	CG	LYS	A	107	38.184	11.361	12.456	1.00	26.56	A
ATOM	71	CD	LYS	A	107	38.430	10.209	13.417	1.00	31.38	A
ATOM	72	CE	LYS	A	107	38.312	10.642	14.868	1.00	35.03	A
ATOM	73	NZ	LYS	A	107	38.599	9.505	15.791	1.00	37.82	A
ATOM	74	C	LYS	A	107	38.359	11.310	8.587	1.00	16.91	A
ATOM	75	O	LYS	A	107	39.446	11.430	8.020	1.00	16.59	A
ATOM	76	N	GLU	A	108	37.345	10.623	8.068	1.00	16.08	A
ATOM	77	CA	GLU	A	108	37.464	9.970	6.770	1.00	16.56	A
ATOM	78	CB	GLU	A	108	36.252	9.072	6.508	1.00	18.83	A
ATOM	79	CG	GLU	A	108	36.214	7.829	7.379	1.00	24.11	A
ATOM	80	CD	GLU	A	108	37.473	6.991	7.241	1.00	29.12	A
ATOM	81	OE1	GLU	A	108	37.798	6.583	6.104	1.00	31.85	A
ATOM	82	OE2	GLU	A	108	38.136	6.742	8.268	1.00	31.72	A
ATOM	83	C	GLU	A	108	37.611	10.973	5.641	1.00	14.32	A
ATOM	84	O	GLU	A	108	38.403	10.768	4.720	1.00	15.54	A
ATOM	85	N	LEU	A	109	36.842	12.057	5.703	1.00	14.02	A
ATOM	86	CA	LEU	A	109	36.920	13.072	4.667	1.00	13.21	A
ATOM	87	CB	LEU	A	109	35.772	14.076	4.823	1.00	14.04	A
ATOM	88	CG	LEU	A	109	35.622	15.125	3.721	1.00	15.48	A
ATOM	89	CD1	LEU	A	109	35.590	14.448	2.353	1.00	17.82	A
ATOM	90	CD2	LEU	A	109	34.345	15.925	3.958	1.00	15.78	A
ATOM	91	C	LEU	A	109	38.280	13.769	4.754	1.00	14.45	A
ATOM	92	O	LEU	A	109	38.896	14.070	3.731	1.00	15.30	A
ATOM	93	N	ASP	A	110	38.751	14.014	5.977	1.00	13.76	A
ATOM	94	CA	ASP	A	110	40.056	14.644	6.170	1.00	14.88	A
ATOM	95	CB	ASP	A	110	40.349	14.864	7.661	1.00	15.02	A
ATOM	96	CG	ASP	A	110	39.606	16.057	8.240	1.00	15.43	A
ATOM	97	OD1	ASP	A	110	38.930	16.782	7.475	1.00	15.66	A
ATOM	98	OD2	ASP	A	110	39.706	16.272	9.471	1.00	15.62	A
ATOM	99	C	ASP	A	110	41.152	13.762	5.566	1.00	15.86	A
ATOM	100	O	ASP	A	110	42.067	14.261	4.910	1.00	15.60	A
ATOM	101	N	LYS	A	111	41.061	12.451	5.788	1.00	17.06	A
ATOM	102	CA	LYS	A	111	42.056	11.528	5.242	1.00	19.14	A
ATOM	103	CB	LYS	A	111	41.773	10.094	5.692	1.00	21.83	A
ATOM	104	CG	LYS	A	111	41.970	9.845	7.176	1.00	28.51	A
ATOM	105	CD	LYS	A	111	41.702	8.384	7.515	1.00	32.83	A
ATOM	106	CE	LYS	A	111	41.819	8.123	9.007	1.00	35.12	A
ATOM	107	NZ	LYS	A	111	41.489	6.707	9.342	1.00	37.22	A
ATOM	108	C	LYS	A	111	42.070	11.585	3.720	1.00	18.08	A
ATOM	109	O	LYS	A	111	43.136	11.599	3.098	1.00	19.72	A
ATOM	110	N	LEU	A	112	40.885	11.616	3.119	1.00	18.52	A
ATOM	111	CA	LEU	A	112	40.771	11.680	1.666	1.00	18.11	A
ATOM	112	CB	LEU	A	112	39.300	11.662	1.244	1.00	18.15	A
ATOM	113	CG	LEU	A	112	39.045	11.712	-.266	1.00	19.29	A
ATOM	114	CD1	LEU	A	112	39.575	10.438	-.906	1.00	20.79	A
ATOM	115	CD2	LEU	A	112	37.556	11.857	-.538	1.00	18.97	A
ATOM	116	C	LEU	A	112	41.424	12.958	1.151	1.00	18.62	A
ATOM	117	O	LEU	A	112	42.010	12.979	.063	1.00	18.72	A
ATOM	118	N	LEU	A	113	41.315	14.021	1.944	1.00	18.70	A
ATOM	119	CA	LEU	A	113	41.879	15.321	1.592	1.00	18.77	A
ATOM	120	CB	LEU	A	113	41.003	16.442	2.160	1.00	18.91	A
ATOM	121	CG	LEU	A	113	39.611	16.587	1.546	1.00	21.50	A
ATOM	122	CD1	LEU	A	113	38.779	17.536	2.391	1.00	21.32	A
ATOM	123	CD2	LEU	A	113	39.735	17.096	.120	1.00	22.16	A
ATOM	124	C	LEU	A	113	43.313	15.493	2.085	1.00	20.09	A
ATOM	125	O	LEU	A	113	43.843	16.606	2.098	1.00	20.28	A
ATOM	126	N	GLN	A	114	43.935	14.392	2.498	1.00	19.91	A
ATOM	127	CA	GLN	A	114	45.313	14.420	2.974	1.00	21.17	A
ATOM	128	CB	GLN	A	114	46.245	14.852	1.841	1.00	22.49	A
ATOM	129	CG	GLN	A	114	46.229	13.937	.635	1.00	23.81	A
ATOM	130	CD	GLN	A	114	47.072	14.475	-.504	1.00	24.77	A
ATOM	131	OE1	GLN	A	114	48.272	14.698	-.351	1.00	27.78	A

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ATOM    132  NE2 GLN A 114      46.444  14.691  -1.653  1.00 26.62      A
ATOM    133  C   GLN A 114      45.521  15.340   4.171  1.00 20.81      A
ATOM    134  O   GLN A 114      46.588  15.938   4.323  1.00 24.10      A
ATOM    135  N   GLY A 115      44.506  15.455   5.019  1.00 18.52      A
ATOM    136  CA  GLY A 115      44.628  16.302   6.189  1.00 19.04      A
ATOM    137  C   GLY A 115      43.440  17.215   6.393  1.00 17.02      A
ATOM    138  O   GLY A 115      43.026  17.462   7.524  1.00 18.66      A
ATOM    139  N   GLY A 116      42.886  17.714   5.292  1.00 15.87      A
ATOM    140  CA  GLY A 116      41.740  18.600   5.372  1.00 14.66      A
ATOM    141  C   GLY A 116      41.760  19.626   4.253  1.00 14.23      A
ATOM    142  O   GLY A 116      42.488  19.462   3.276  1.00 14.98      A
ATOM    143  N   ILE A 117      40.967  20.683   4.393  1.00 12.49      A
ATOM    144  CA  ILE A 117      40.907  21.738   3.384  1.00 11.37      A
ATOM    145  CB  ILE A 117      39.677  22.639   3.619  1.00 10.73      A
ATOM    146  CG2 ILE A 117      39.706  23.836   2.676  1.00 12.58      A
ATOM    147  CG1 ILE A 117      38.396  21.819   3.429  1.00 12.81      A
ATOM    148  CD1 ILE A 117      38.180  21.302   2.016  1.00 14.44      A
ATOM    149  C   ILE A 117      42.195  22.559   3.428  1.00 10.95      A
ATOM    150  O   ILE A 117      42.578  23.093   4.466  1.00 12.19      A
ATOM    151  N   GLU A 118      42.849  22.665   2.277  1.00 10.51      A
ATOM    152  CA  GLU A 118      44.132  23.343   2.151  1.00 12.58      A
ATOM    153  CB  GLU A 118      44.870  22.714    .968  1.00 15.64      A
ATOM    154  CG  GLU A 118      46.365  22.783   1.022  1.00 21.41      A
ATOM    155  CD  GLU A 118      46.996  21.963   -.085  1.00 20.95      A
ATOM    156  OE1 GLU A 118      47.180  22.499  -1.194  1.00 23.24      A
ATOM    157  OE2 GLU A 118      47.284  20.773    .156  1.00 26.48      A
ATOM    158  C   GLU A 118      44.120  24.861   1.982  1.00 12.88      A
ATOM    159  O   GLU A 118      43.449  25.384   1.098  1.00 12.57      A
ATOM    160  N   THR A 119      44.872  25.569   2.822  1.00 11.45      A
ATOM    161  CA  THR A 119      44.962  27.017   2.681  1.00 11.27      A
ATOM    162  CB  THR A 119      45.553  27.700   3.946  1.00 11.65      A
ATOM    163  OG1 THR A 119      46.863  27.180   4.220  1.00 12.69      A
ATOM    164  CG2 THR A 119      44.650  27.468   5.149  1.00 11.67      A
ATOM    165  C   THR A 119      45.891  27.282   1.492  1.00 11.98      A
ATOM    166  O   THR A 119      46.769  26.467   1.194  1.00 12.27      A
ATOM    167  N   GLY A 120      45.679  28.397    .798  1.00 10.27      A
ATOM    168  CA  GLY A 120      46.526  28.740   -.333  1.00 10.55      A
ATOM    169  C   GLY A 120      46.071  28.245  -1.690  1.00 10.39      A
ATOM    170  O   GLY A 120      46.737  28.490  -2.700  1.00 11.43      A
ATOM    171  N   SER A 121      44.948  27.534  -1.726  1.00 10.13      A
ATOM    172  CA  SER A 121      44.423  27.028  -2.984  1.00  9.86      A
ATOM    173  CB  SER A 121      45.008  25.645  -3.299  1.00 13.87      A
ATOM    174  OG  SER A 121      44.622  24.700  -2.326  1.00 19.34      A
ATOM    175  C   SER A 121      42.904  26.947  -2.918  1.00  9.08      A
ATOM    176  O   SER A 121      42.302  27.194  -1.875  1.00  8.68      A
ATOM    177  N   ILE A 122      42.298  26.611  -4.048  1.00  9.44      A
ATOM    178  CA  ILE A 122      40.854  26.503  -4.154  1.00 10.10      A
ATOM    179  CB  ILE A 122      40.360  27.090  -5.505  1.00 10.40      A
ATOM    180  CG2 ILE A 122      38.858  26.863  -5.663  1.00 12.37      A
ATOM    181  CG1 ILE A 122      40.702  28.579  -5.586  1.00 13.97      A
ATOM    182  CD1 ILE A 122      40.453  29.187  -6.952  1.00 14.82      A
ATOM    183  C   ILE A 122      40.381  25.056  -4.072  1.00 11.37      A
ATOM    184  O   ILE A 122      40.982  24.162  -4.666  1.00 12.71      A
ATOM    185  N   THR A 123      39.323  24.832  -3.304  1.00  9.56      A
ATOM    186  CA  THR A 123      38.708  23.513  -3.212  1.00  9.79      A
ATOM    187  CB  THR A 123      38.526  23.041  -1.760  1.00 10.66      A
ATOM    188  OG1 THR A 123      39.811  22.851  -1.158  1.00 13.42      A
ATOM    189  CG2 THR A 123      37.751  21.719  -1.724  1.00 10.55      A
ATOM    190  C   THR A 123      37.339  23.769  -3.827  1.00  8.71      A
ATOM    191  O   THR A 123      36.581  24.603  -3.329  1.00 10.46      A
ATOM    192  N   GLU A 124      37.041  23.084  -4.926  1.00  9.35      A
ATOM    193  CA  GLU A 124      35.770  23.256  -5.624  1.00  9.53      A
ATOM    194  CB  GLU A 124      36.043  23.472  -7.115  1.00 12.39      A
ATOM    195  CG  GLU A 124      34.820  23.549  -8.006  1.00 13.73      A
ATOM    196  CD  GLU A 124      35.199  23.914  -9.429  1.00 17.73      A
ATOM    197  OE1 GLU A 124      36.273  23.462  -9.887  1.00 16.72      A
ATOM    198  OE2 GLU A 124      34.428  24.647 -10.086  1.00 18.68      A
ATOM    199  C   GLU A 124      34.900  22.025  -5.399  1.00 10.21      A
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ATOM    200  O   GLU A 124      35.283  20.911  -5.749  1.00 10.78      A
ATOM    201  N   MSE A 125      33.729  22.239  -4.807  1.00 10.59      A
ATOM    202  CA  MSE A 125      32.825  21.143  -4.495  1.00 11.22      A
ATOM    203  CB  MSE A 125      32.413  21.237  -3.028  1.00 13.67      A
ATOM    204  CG  MSE A 125      33.605  21.453  -2.110  1.00 14.05      A
ATOM    205  SE  MSE A 125      33.164  21.237   -.250  1.00 21.89      A
ATOM    206  CE  MSE A 125      31.991  22.745   -.036  1.00 16.55      A
ATOM    207  C   MSE A 125      31.595  21.128  -5.387  1.00 12.28      A
ATOM    208  O   MSE A 125      30.878  22.123  -5.495  1.00 12.87      A
ATOM    209  N   PHE A 126      31.361  19.986  -6.026  1.00 13.37      A
ATOM    210  CA  PHE A 126      30.220  19.829  -6.917  1.00 14.46      A
ATOM    211  CB  PHE A 126      30.634  19.085  -8.185  1.00 13.72      A
ATOM    212  CG  PHE A 126      31.575  19.857  -9.059  1.00 15.70      A
ATOM    213  CD1 PHE A 126      32.938  19.890  -8.783  1.00 16.05      A
ATOM    214  CD2 PHE A 126      31.095  20.565 -10.155  1.00 15.36      A
ATOM    215  CE1 PHE A 126      33.811  20.619  -9.588  1.00 16.76      A
ATOM    216  CE2 PHE A 126      31.961  21.297 -10.966  1.00 16.46      A
ATOM    217  CZ  PHE A 126      33.320  21.323 -10.682  1.00 15.73      A
ATOM    218  C   PHE A 126      29.078  19.083  -6.252  1.00 16.95      A
ATOM    219  O   PHE A 126      29.292  18.071  -5.589  1.00 16.20      A
ATOM    220  N   GLY A 127      27.866  19.597  -6.442  1.00 19.76      A
ATOM    221  CA  GLY A 127      26.683  18.983  -5.866  1.00 22.59      A
ATOM    222  C   GLY A 127      25.608  20.006  -5.542  1.00 24.79      A
ATOM    223  O   GLY A 127      25.904  21.181  -5.300  1.00 24.48      A
ATOM    224  N   GLU A 128      24.354  19.561  -5.535  1.00 27.02      A
ATOM    225  CA  GLU A 128      23.230  20.442  -5.228  1.00 28.56      A
ATOM    226  CB  GLU A 128      21.929  19.863  -5.787  1.00 31.81      A
ATOM    227  CG  GLU A 128      21.852  19.818  -7.305  1.00 36.61      A
ATOM    228  CD  GLU A 128      21.889  21.199  -7.932  1.00 39.77      A
ATOM    229  OE1 GLU A 128      21.116  22.075  -7.487  1.00 42.32      A
ATOM    230  OE2 GLU A 128      22.685  21.410  -8.874  1.00 41.49      A
ATOM    231  C   GLU A 128      23.089  20.606  -3.721  1.00 27.92      A
ATOM    232  O   GLU A 128      23.714  19.878  -2.949  1.00 27.36      A
ATOM    233  N   PHE A 129      22.269  21.567  -3.306  1.00 26.59      A
ATOM    234  CA  PHE A 129      22.044  21.794  -1.887  1.00 26.34      A
ATOM    235  CB  PHE A 129      20.979  22.879  -1.682  1.00 26.99      A
ATOM    236  CG  PHE A 129      20.628  23.128   -.238  1.00 27.71      A
ATOM    237  CD1 PHE A 129      21.607  23.501    .678  1.00 26.29      A
ATOM    238  CD2 PHE A 129      19.311  23.006    .203  1.00 27.59      A
ATOM    239  CE1 PHE A 129      21.284  23.751   2.013  1.00 27.10      A
ATOM    240  CE2 PHE A 129      18.976  23.253   1.537  1.00 27.95      A
ATOM    241  CZ  PHE A 129      19.966  23.627   2.443  1.00 28.18      A
ATOM    242  C   PHE A 129      21.567  20.467  -1.312  1.00 26.38      A
ATOM    243  O   PHE A 129      20.789  19.756  -1.949  1.00 26.54      A
ATOM    244  N   ARG A 130      22.062  20.138   -.124  1.00 25.28      A
ATOM    245  CA  ARG A 130      21.727  18.909    .589  1.00 24.10      A
ATOM    246  CB  ARG A 130      20.270  18.507    .331  1.00 27.41      A
ATOM    247  CG  ARG A 130      19.291  19.529    .893  1.00 32.24      A
ATOM    248  CD  ARG A 130      17.866  19.017    .958  1.00 38.42      A
ATOM    249  NE  ARG A 130      17.058  19.876   1.820  1.00 44.65      A
ATOM    250  CZ  ARG A 130      15.787  19.650   2.135  1.00 48.26      A
ATOM    251  NH1 ARG A 130      15.160  18.583   1.657  1.00 50.05      A
ATOM    252  NH2 ARG A 130      15.144  20.490   2.937  1.00 49.61      A
ATOM    253  C   ARG A 130      22.666  17.735    .327  1.00 21.02      A
ATOM    254  O   ARG A 130      22.608  16.737   1.035  1.00 20.30      A
ATOM    255  N   THR A 131      23.530  17.846   -.680  1.00 19.13      A
ATOM    256  CA  THR A 131      24.490  16.776   -.955  1.00 17.15      A
ATOM    257  CB  THR A 131      25.129  16.904  -2.351  1.00 19.70      A
ATOM    258  OG1 THR A 131      25.761  18.184  -2.469  1.00 21.01      A
ATOM    259  CG2 THR A 131      24.079  16.744  -3.439  1.00 22.19      A
ATOM    260  C   THR A 131      25.601  16.899    .082  1.00 16.43      A
ATOM    261  O   THR A 131      26.455  16.020    .212  1.00 15.57      A
ATOM    262  N   GLY A 132      25.583  18.012    .810  1.00 15.23      A
ATOM    263  CA  GLY A 132      26.581  18.246   1.836  1.00 14.02      A
ATOM    264  C   GLY A 132      27.459  19.463   1.598  1.00 13.72      A
ATOM    265  O   GLY A 132      28.118  19.935   2.524  1.00 13.81      A
ATOM    266  N   LYS A 133      27.467  19.986    .374  1.00 12.58      A
ATOM    267  CA  LYS A 133      28.306  21.140    .060  1.00 12.45      A
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ATOM	268	CB	LYS	A	133	28.111	21.557	-1.408	1.00	13.99	A
ATOM	269	CG	LYS	A	133	26.687	21.910	-1.804	1.00	16.59	A
ATOM	270	CD	LYS	A	133	26.511	23.414	-1.951	1.00	19.12	A
ATOM	271	CE	LYS	A	133	25.098	23.756	-2.398	1.00	21.74	A
ATOM	272	NZ	LYS	A	133	24.906	25.222	-2.577	1.00	23.48	A
ATOM	273	C	LYS	A	133	28.111	22.343	.990	1.00	11.78	A
ATOM	274	O	LYS	A	133	29.084	22.923	1.476	1.00	12.85	A
ATOM	275	N	THR	A	134	26.866	22.718	1.250	1.00	12.16	A
ATOM	276	CA	THR	A	134	26.615	23.856	2.123	1.00	12.03	A
ATOM	277	CB	THR	A	134	25.169	24.366	1.959	1.00	12.33	A
ATOM	278	OG1	THR	A	134	24.999	24.861	.622	1.00	14.07	A
ATOM	279	CG2	THR	A	134	24.874	25.485	2.950	1.00	14.49	A
ATOM	280	C	THR	A	134	26.892	23.515	3.585	1.00	11.44	A
ATOM	281	O	THR	A	134	27.315	24.380	4.357	1.00	11.86	A
ATOM	282	N	GLN	A	135	26.668	22.260	3.964	1.00	11.19	A
ATOM	283	CA	GLN	A	135	26.920	21.833	5.339	1.00	9.68	A
ATOM	284	CB	GLN	A	135	26.391	20.419	5.581	1.00	12.98	A
ATOM	285	CG	GLN	A	135	24.923	20.247	5.243	1.00	15.40	A
ATOM	286	CD	GLN	A	135	24.058	21.355	5.807	1.00	19.13	A
ATOM	287	OE1	GLN	A	135	23.318	22.011	5.071	1.00	22.64	A
ATOM	288	NE2	GLN	A	135	24.141	21.570	7.115	1.00	16.98	A
ATOM	289	C	GLN	A	135	28.420	21.868	5.605	1.00	10.76	A
ATOM	290	O	GLN	A	135	28.859	22.279	6.679	1.00	9.99	A
ATOM	291	N	ILE	A	136	29.204	21.432	4.624	1.00	9.71	A
ATOM	292	CA	ILE	A	136	30.655	21.449	4.761	1.00	10.04	A
ATOM	293	CB	ILE	A	136	31.345	20.817	3.528	1.00	9.93	A
ATOM	294	CG2	ILE	A	136	32.840	21.125	3.548	1.00	12.14	A
ATOM	295	CG1	ILE	A	136	31.113	19.303	3.528	1.00	12.11	A
ATOM	296	CD1	ILE	A	136	31.574	18.602	2.263	1.00	10.81	A
ATOM	297	C	ILE	A	136	31.112	22.896	4.924	1.00	10.64	A
ATOM	298	O	ILE	A	136	31.962	23.195	5.764	1.00	9.71	A
ATOM	299	N	CYS	A	137	30.537	23.796	4.129	1.00	10.36	A
ATOM	300	CA	CYS	A	137	30.896	25.209	4.210	1.00	10.00	A
ATOM	301	CB	CYS	A	137	30.135	26.025	3.164	1.00	8.86	A
ATOM	302	SG	CYS	A	137	30.711	25.760	1.458	1.00	13.33	A
ATOM	303	C	CYS	A	137	30.620	25.777	5.598	1.00	7.98	A
ATOM	304	O	CYS	A	137	31.448	26.500	6.151	1.00	10.27	A
ATOM	305	N	HIS	A	138	29.461	25.456	6.165	1.00	8.44	A
ATOM	306	CA	HIS	A	138	29.131	25.960	7.493	1.00	7.87	A
ATOM	307	CB	HIS	A	138	27.675	25.634	7.864	1.00	9.77	A
ATOM	308	CG	HIS	A	138	26.672	26.585	7.280	1.00	9.79	A
ATOM	309	CD2	HIS	A	138	25.904	27.537	7.861	1.00	10.42	A
ATOM	310	ND1	HIS	A	138	26.385	26.629	5.933	1.00	10.42	A
ATOM	311	CE1	HIS	A	138	25.482	27.570	5.708	1.00	12.62	A
ATOM	312	NE2	HIS	A	138	25.175	28.136	6.860	1.00	10.74	A
ATOM	313	C	HIS	A	138	30.070	25.384	8.549	1.00	8.06	A
ATOM	314	O	HIS	A	138	30.481	26.091	9.465	1.00	9.19	A
ATOM	315	N	THR	A	139	30.412	24.107	8.422	1.00	7.84	A
ATOM	316	CA	THR	A	139	31.306	23.489	9.395	1.00	8.21	A
ATOM	317	CB	THR	A	139	31.439	21.970	9.154	1.00	9.18	A
ATOM	318	OG1	THR	A	139	30.147	21.358	9.273	1.00	11.07	A
ATOM	319	CG2	THR	A	139	32.372	21.344	10.186	1.00	9.48	A
ATOM	320	C	THR	A	139	32.684	24.151	9.336	1.00	8.27	A
ATOM	321	O	THR	A	139	33.249	24.504	10.365	1.00	8.65	A
ATOM	322	N	LEU	A	140	33.208	24.328	8.126	1.00	6.73	A
ATOM	323	CA	LEU	A	140	34.516	24.952	7.936	1.00	7.10	A
ATOM	324	CB	LEU	A	140	34.900	24.938	6.454	1.00	6.22	A
ATOM	325	CG	LEU	A	140	35.191	23.585	5.806	1.00	7.89	A
ATOM	326	CD1	LEU	A	140	35.368	23.765	4.298	1.00	9.36	A
ATOM	327	CD2	LEU	A	140	36.446	22.975	6.425	1.00	10.17	A
ATOM	328	C	LEU	A	140	34.572	26.389	8.447	1.00	8.54	A
ATOM	329	O	LEU	A	140	35.629	26.856	8.879	1.00	8.74	A
ATOM	330	N	ALA	A	141	33.444	27.094	8.380	1.00	8.10	A
ATOM	331	CA	ALA	A	141	33.397	28.479	8.840	1.00	7.81	A
ATOM	332	CB	ALA	A	141	32.044	29.098	8.513	1.00	7.95	A
ATOM	333	C	ALA	A	141	33.664	28.551	10.339	1.00	8.11	A
ATOM	334	O	ALA	A	141	34.018	29.612	10.871	1.00	8.73	A
ATOM	335	N	VAL	A	142	33.488	27.419	11.018	1.00	7.57	A

ATOM	336	CA	VAL	A	142	33.746	27.349	12.450	1.00	8.68	A
ATOM	337	CB	VAL	A	142	32.628	26.579	13.187	1.00	8.53	A
ATOM	338	CG1	VAL	A	142	32.926	26.526	14.693	1.00	9.23	A
ATOM	339	CG2	VAL	A	142	31.292	27.270	12.946	1.00	9.18	A
ATOM	340	C	VAL	A	142	35.087	26.674	12.742	1.00	8.97	A
ATOM	341	O	VAL	A	142	35.889	27.197	13.517	1.00	10.90	A
ATOM	342	N	THR	A	143	35.345	25.525	12.121	1.00	9.37	A
ATOM	343	CA	THR	A	143	36.601	24.819	12.378	1.00	9.23	A
ATOM	344	CB	THR	A	143	36.637	23.422	11.716	1.00	9.23	A
ATOM	345	OG1	THR	A	143	36.497	23.550	10.295	1.00	9.23	A
ATOM	346	CG2	THR	A	143	35.521	22.546	12.274	1.00	9.22	A
ATOM	347	C	THR	A	143	37.839	25.591	11.945	1.00	9.03	A
ATOM	348	O	THR	A	143	38.929	25.348	12.456	1.00	10.11	A
ATOM	349	N	CYS	A	144	37.688	26.522	11.010	1.00	8.10	A
ATOM	350	CA	CYS	A	144	38.848	27.294	10.580	1.00	9.39	A
ATOM	351	CB	CYS	A	144	38.514	28.139	9.345	1.00	9.38	A
ATOM	352	SG	CYS	A	144	37.374	29.498	9.667	1.00	12.00	A
ATOM	353	C	CYS	A	144	39.315	28.200	11.719	1.00	9.07	A
ATOM	354	O	CYS	A	144	40.447	28.680	11.712	1.00	10.50	A
ATOM	355	N	GLN	A	145	38.447	28.403	12.709	1.00	8.72	A
ATOM	356	CA	GLN	A	145	38.755	29.256	13.858	1.00	10.01	A
ATOM	357	CB	GLN	A	145	37.465	29.865	14.403	1.00	10.49	A
ATOM	358	CG	GLN	A	145	36.725	30.720	13.387	1.00	11.33	A
ATOM	359	CD	GLN	A	145	35.499	31.375	13.976	1.00	13.67	A
ATOM	360	OE1	GLN	A	145	35.543	31.907	15.086	1.00	14.78	A
ATOM	361	NE2	GLN	A	145	34.398	31.355	13.234	1.00	10.01	A
ATOM	362	C	GLN	A	145	39.477	28.521	14.985	1.00	10.04	A
ATOM	363	O	GLN	A	145	39.982	29.143	15.926	1.00	11.00	A
ATOM	364	N	LEU	A	146	39.524	27.198	14.886	1.00	9.00	A
ATOM	365	CA	LEU	A	146	40.179	26.373	15.898	1.00	10.62	A
ATOM	366	CB	LEU	A	146	39.875	24.893	15.653	1.00	10.21	A
ATOM	367	CG	LEU	A	146	38.469	24.337	15.874	1.00	11.36	A
ATOM	368	CD1	LEU	A	146	38.393	22.952	15.256	1.00	11.83	A
ATOM	369	CD2	LEU	A	146	38.151	24.280	17.365	1.00	15.14	A
ATOM	370	C	LEU	A	146	41.692	26.528	15.932	1.00	11.26	A
ATOM	371	O	LEU	A	146	42.309	26.979	14.968	1.00	11.50	A
ATOM	372	N	PRO	A	147	42.309	26.178	17.070	1.00	12.58	A
ATOM	373	CD	PRO	A	147	41.680	25.866	18.367	1.00	12.30	A
ATOM	374	CA	PRO	A	147	43.764	26.265	17.202	1.00	11.87	A
ATOM	375	CB	PRO	A	147	44.010	25.732	18.608	1.00	13.51	A
ATOM	376	CG	PRO	A	147	42.792	26.180	19.349	1.00	13.16	A
ATOM	377	C	PRO	A	147	44.320	25.316	16.139	1.00	11.90	A
ATOM	378	O	PRO	A	147	43.670	24.321	15.796	1.00	12.36	A
ATOM	379	N	ILE	A	148	45.505	25.602	15.620	1.00	12.68	A
ATOM	380	CA	ILE	A	148	46.072	24.736	14.596	1.00	13.79	A
ATOM	381	CB	ILE	A	148	47.433	25.279	14.105	1.00	15.52	A
ATOM	382	CG2	ILE	A	148	48.074	24.290	13.141	1.00	16.43	A
ATOM	383	CG1	ILE	A	148	47.216	26.625	13.397	1.00	19.02	A
ATOM	384	CD1	ILE	A	148	48.492	27.326	12.980	1.00	23.77	A
ATOM	385	C	ILE	A	148	46.212	23.285	15.060	1.00	12.90	A
ATOM	386	O	ILE	A	148	45.996	22.361	14.277	1.00	12.36	A
ATOM	387	N	ASP	A	149	46.538	23.074	16.335	1.00	13.06	A
ATOM	388	CA	ASP	A	149	46.687	21.708	16.833	1.00	13.17	A
ATOM	389	CB	ASP	A	149	47.367	21.698	18.213	1.00	14.99	A
ATOM	390	CG	ASP	A	149	46.454	22.178	19.326	1.00	15.68	A
ATOM	391	OD1	ASP	A	149	46.334	23.404	19.522	1.00	15.33	A
ATOM	392	OD2	ASP	A	149	45.856	21.318	20.005	1.00	18.19	A
ATOM	393	C	ASP	A	149	45.368	20.926	16.894	1.00	14.26	A
ATOM	394	O	ASP	A	149	45.374	19.700	17.034	1.00	14.29	A
ATOM	395	N	ARG	A	150	44.237	21.624	16.789	1.00	11.56	A
ATOM	396	CA	ARG	A	150	42.940	20.954	16.810	1.00	12.66	A
ATOM	397	CB	ARG	A	150	41.936	21.724	17.676	1.00	13.00	A
ATOM	398	CG	ARG	A	150	42.306	21.817	19.157	1.00	13.36	A
ATOM	399	CD	ARG	A	150	41.143	22.378	19.964	1.00	12.59	A
ATOM	400	NE	ARG	A	150	40.019	21.444	19.975	1.00	12.66	A
ATOM	401	CZ	ARG	A	150	38.785	21.745	20.369	1.00	13.24	A
ATOM	402	NH1	ARG	A	150	38.494	22.967	20.791	1.00	13.27	A
ATOM	403	NH2	ARG	A	150	37.838	20.815	20.338	1.00	13.59	A

ATOM	404	C	ARG	A	150	42.391	20.819	15.390	1.00	13.09	A
ATOM	405	O	ARG	A	150	41.246	20.404	15.195	1.00	13.09	A
ATOM	406	N	GLY	A	151	43.212	21.183	14.407	1.00	12.45	A
ATOM	407	CA	GLY	A	151	42.797	21.082	13.017	1.00	12.19	A
ATOM	408	C	GLY	A	151	42.254	22.366	12.423	1.00	11.65	A
ATOM	409	O	GLY	A	151	41.647	22.354	11.353	1.00	12.49	A
ATOM	410	N	GLY	A	152	42.472	23.484	13.106	1.00	11.30	A
ATOM	411	CA	GLY	A	152	41.969	24.747	12.599	1.00	10.67	A
ATOM	412	C	GLY	A	152	43.004	25.589	11.885	1.00	11.78	A
ATOM	413	O	GLY	A	152	44.135	25.155	11.659	1.00	10.04	A
ATOM	414	N	GLY	A	153	42.603	26.805	11.522	1.00	11.68	A
ATOM	415	CA	GLY	A	153	43.504	27.713	10.842	1.00	12.29	A
ATOM	416	C	GLY	A	153	43.735	28.967	11.661	1.00	11.95	A
ATOM	417	O	GLY	A	153	44.413	29.892	11.210	1.00	14.26	A
ATOM	418	N	GLU	A	154	43.178	28.991	12.870	1.00	13.09	A
ATOM	419	CA	GLU	A	154	43.310	30.138	13.765	1.00	13.65	A
ATOM	420	CB	GLU	A	154	44.722	30.185	14.359	1.00	15.09	A
ATOM	421	CG	GLU	A	154	44.924	29.184	15.479	1.00	17.51	A
ATOM	422	CD	GLU	A	154	46.372	29.050	15.907	1.00	21.30	A
ATOM	423	OE1	GLU	A	154	47.095	30.070	15.921	1.00	21.05	A
ATOM	424	OE2	GLU	A	154	46.779	27.920	16.244	1.00	21.68	A
ATOM	425	C	GLU	A	154	43.000	31.447	13.045	1.00	13.66	A
ATOM	426	O	GLU	A	154	43.714	32.439	13.193	1.00	15.59	A
ATOM	427	N	GLY	A	155	41.921	31.444	12.271	1.00	12.01	A
ATOM	428	CA	GLY	A	155	41.549	32.638	11.540	1.00	11.09	A
ATOM	429	C	GLY	A	155	40.055	32.792	11.354	1.00	11.53	A
ATOM	430	O	GLY	A	155	39.278	31.872	11.616	1.00	10.72	A
ATOM	431	N	LYS	A	156	39.654	33.976	10.903	1.00	11.50	A
ATOM	432	CA	LYS	A	156	38.252	34.277	10.655	1.00	11.09	A
ATOM	433	CB	LYS	A	156	38.048	35.789	10.561	1.00	11.40	A
ATOM	434	CG	LYS	A	156	38.265	36.533	11.863	1.00	14.73	A
ATOM	435	CD	LYS	A	156	38.168	38.031	11.616	1.00	18.50	A
ATOM	436	CE	LYS	A	156	38.158	38.814	12.916	1.00	21.90	A
ATOM	437	NZ	LYS	A	156	38.016	40.271	12.640	1.00	26.01	A
ATOM	438	C	LYS	A	156	37.789	33.643	9.352	1.00	10.36	A
ATOM	439	O	LYS	A	156	38.599	33.213	8.529	1.00	9.77	A
ATOM	440	N	ALA	A	157	36.477	33.593	9.168	1.00	9.56	A
ATOM	441	CA	ALA	A	157	35.919	33.037	7.949	1.00	8.82	A
ATOM	442	CB	ALA	A	157	35.042	31.831	8.262	1.00	9.17	A
ATOM	443	C	ALA	A	157	35.093	34.085	7.234	1.00	10.33	A
ATOM	444	O	ALA	A	157	34.468	34.942	7.860	1.00	10.06	A
ATOM	445	N	MSE		158	35.099	34.006	5.912	.54	9.17	AC1
ATOM	446	CA	MSE		158	34.321	34.913	5.097	.54	10.42	AC1
ATOM	447	CB	MSE		158	35.231	35.701	4.174	.54	11.72	AC1
ATOM	448	CG	MSE		158	34.551	36.879	3.548	.54	13.13	AC1
ATOM	449	SE	MSE		158	35.839	37.882	2.572	.54	15.92	AC1
ATOM	450	CE	MSE		158	37.003	38.379	4.022	.54	11.46	AC1
ATOM	451	C	MSE		158	33.391	34.013	4.298	.54	10.25	AC1
ATOM	452	O	MSE		158	33.830	33.034	3.694	.54	10.22	AC1
ATOM	453	N	TYR	A	159	32.106	34.343	4.304	1.00	10.25	A
ATOM	454	CA	TYR	A	159	31.111	33.534	3.616	1.00	10.01	A
ATOM	455	CB	TYR	A	159	30.201	32.892	4.676	1.00	9.57	A
ATOM	456	CG	TYR	A	159	29.410	31.677	4.242	1.00	10.37	A
ATOM	457	CD1	TYR	A	159	28.533	31.730	3.158	1.00	11.98	A
ATOM	458	CE1	TYR	A	159	27.786	30.609	2.783	1.00	13.38	A
ATOM	459	CD2	TYR	A	159	29.520	30.474	4.943	1.00	11.85	A
ATOM	460	CE2	TYR	A	159	28.777	29.350	4.576	1.00	11.39	A
ATOM	461	CZ	TYR	A	159	27.914	29.425	3.498	1.00	13.64	A
ATOM	462	OH	TYR	A	159	27.187	28.315	3.136	1.00	14.59	A
ATOM	463	C	TYR	A	159	30.267	34.333	2.630	1.00	10.25	A
ATOM	464	O	TYR	A	159	29.432	35.139	3.038	1.00	10.49	A
ATOM	465	N	ILE	A	160	30.490	34.115	1.336	1.00	9.28	A
ATOM	466	CA	ILE	A	160	29.705	34.792	.314	1.00	9.69	A
ATOM	467	CB	ILE	A	160	30.568	35.214	-.896	1.00	9.03	A
ATOM	468	CG2	ILE	A	160	29.678	35.780	-1.999	1.00	13.08	A
ATOM	469	CG1	ILE	A	160	31.592	36.265	-.458	1.00	10.09	A
ATOM	470	CD1	ILE	A	160	32.556	36.699	-1.554	1.00	8.81	A
ATOM	471	C	ILE	A	160	28.645	33.794	-.135	1.00	10.60	A

ATOM	472	O	ILE	A	160	28.960	32.751	-.708	1.00	10.08	A
ATOM	473	N	ASP	A	161	27.390	34.117	.155	1.00	11.32	A
ATOM	474	CA	ASP	A	161	26.263	33.260	-.192	1.00	12.57	A
ATOM	475	CB	ASP	A	161	25.293	33.175	.994	1.00	13.81	A
ATOM	476	CG	ASP	A	161	23.963	32.540	.619	1.00	16.41	A
ATOM	477	OD1	ASP	A	161	23.936	31.323	.345	1.00	17.20	A
ATOM	478	OD2	ASP	A	161	22.945	33.267	.589	1.00	19.96	A
ATOM	479	C	ASP	A	161	25.520	33.815	-1.399	1.00	13.45	A
ATOM	480	O	ASP	A	161	25.437	35.027	-1.577	1.00	15.58	A
ATOM	481	N	THR	A	162	24.984	32.925	-2.226	1.00	15.93	A
ATOM	482	CA	THR	A	162	24.221	33.347	-3.396	1.00	16.70	A
ATOM	483	CB	THR	A	162	24.949	33.011	-4.718	1.00	16.70	A
ATOM	484	OG1	THR	A	162	24.979	31.588	-4.897	1.00	17.06	A
ATOM	485	CG2	THR	A	162	26.371	33.555	-4.708	1.00	16.05	A
ATOM	486	C	THR	A	162	22.898	32.594	-3.409	1.00	18.68	A
ATOM	487	O	THR	A	162	22.012	32.894	-4.212	1.00	19.52	A
ATOM	488	N	GLU	A	163	22.771	31.629	-2.501	1.00	18.38	A
ATOM	489	CA	GLU	A	163	21.589	30.772	-2.425	1.00	20.29	A
ATOM	490	CB	GLU	A	163	22.031	29.318	-2.260	1.00	20.64	A
ATOM	491	CG	GLU	A	163	23.048	28.837	-3.278	1.00	25.07	A
ATOM	492	CD	GLU	A	163	22.527	28.909	-4.696	1.00	27.45	A
ATOM	493	OE1	GLU	A	163	22.624	29.991	-5.315	1.00	26.80	A
ATOM	494	OE2	GLU	A	163	22.009	27.883	-5.184	1.00	28.60	A
ATOM	495	C	GLU	A	163	20.573	31.078	-1.332	1.00	20.03	A
ATOM	496	O	GLU	A	163	19.466	30.539	-1.354	1.00	21.59	A
ATOM	497	N	GLY	A	164	20.948	31.915	-.372	1.00	19.41	A
ATOM	498	CA	GLY	A	164	20.043	32.234	.718	1.00	19.90	A
ATOM	499	C	GLY	A	164	19.981	31.097	1.723	1.00	19.77	A
ATOM	500	O	GLY	A	164	18.979	30.919	2.419	1.00	19.85	A
ATOM	501	N	THR	A	165	21.059	30.323	1.807	1.00	15.75	A
ATOM	502	CA	THR	A	165	21.106	29.193	2.729	1.00	16.97	A
ATOM	503	CB	THR	A	165	21.388	27.879	1.973	1.00	16.58	A
ATOM	504	OG1	THR	A	165	22.474	28.074	1.057	1.00	16.41	A
ATOM	505	CG2	THR	A	165	20.149	27.435	1.205	1.00	19.06	A
ATOM	506	C	THR	A	165	22.117	29.344	3.864	1.00	16.78	A
ATOM	507	O	THR	A	165	22.512	28.359	4.492	1.00	16.85	A
ATOM	508	N	PHE	A	166	22.543	30.574	4.125	1.00	15.79	A
ATOM	509	CA	PHE	A	166	23.477	30.820	5.217	1.00	14.36	A
ATOM	510	CB	PHE	A	166	24.153	32.181	5.058	1.00	13.90	A
ATOM	511	CG	PHE	A	166	25.137	32.498	6.154	1.00	13.95	A
ATOM	512	CD1	PHE	A	166	26.357	31.829	6.230	1.00	13.42	A
ATOM	513	CD2	PHE	A	166	24.840	33.462	7.115	1.00	13.77	A
ATOM	514	CE1	PHE	A	166	27.270	32.119	7.248	1.00	13.37	A
ATOM	515	CE2	PHE	A	166	25.744	33.759	8.135	1.00	13.84	A
ATOM	516	CZ	PHE	A	166	26.963	33.086	8.202	1.00	14.21	A
ATOM	517	C	PHE	A	166	22.650	30.805	6.498	1.00	16.02	A
ATOM	518	O	PHE	A	166	21.637	31.502	6.592	1.00	15.82	A
ATOM	519	N	ARG	A	167	23.073	30.018	7.482	1.00	14.61	A
ATOM	520	CA	ARG	A	167	22.333	29.919	8.738	1.00	15.67	A
ATOM	521	CB	ARG	A	167	21.574	28.590	8.785	1.00	17.46	A
ATOM	522	CG	ARG	A	167	20.523	28.425	7.695	1.00	21.67	A
ATOM	523	CD	ARG	A	167	19.307	29.307	7.944	1.00	26.33	A
ATOM	524	NE	ARG	A	167	18.267	29.086	6.940	1.00	30.64	A
ATOM	525	CZ	ARG	A	167	18.256	29.639	5.731	1.00	32.90	A
ATOM	526	NH1	ARG	A	167	19.229	30.462	5.362	1.00	32.52	A
ATOM	527	NH2	ARG	A	167	17.272	29.362	4.884	1.00	34.53	A
ATOM	528	C	ARG	A	167	23.206	30.046	9.984	1.00	14.69	A
ATOM	529	O	ARG	A	167	23.897	29.099	10.375	1.00	13.43	A
ATOM	530	N	PRO	A	168	23.186	31.223	10.627	1.00	14.89	A
ATOM	531	CD	PRO	A	168	22.557	32.476	10.172	1.00	14.33	A
ATOM	532	CA	PRO	A	168	23.984	31.445	11.836	1.00	15.39	A
ATOM	533	CB	PRO	A	168	23.561	32.846	12.273	1.00	14.97	A
ATOM	534	CG	PRO	A	168	23.315	33.530	10.956	1.00	15.63	A
ATOM	535	C	PRO	A	168	23.738	30.391	12.919	1.00	16.84	A
ATOM	536	O	PRO	A	168	24.656	30.028	13.654	1.00	16.46	A
ATOM	537	N	GLU	A	169	22.508	29.887	13.015	1.00	17.31	A
ATOM	538	CA	GLU	A	169	22.208	28.886	14.036	1.00	18.18	A
ATOM	539	CB	GLU	A	169	20.714	28.538	14.055	1.00	21.53	A

ATOM	540	CG	GLU	A	169	20.140	28.117	12.717	1.00	26.55	A
ATOM	541	CD	GLU	A	169	19.394	29.242	12.019	1.00	30.20	A
ATOM	542	OE1	GLU	A	169	19.999	30.309	11.762	1.00	27.11	A
ATOM	543	OE2	GLU	A	169	18.194	29.050	11.728	1.00	32.63	A
ATOM	544	C	GLU	A	169	23.029	27.614	13.861	1.00	16.74	A
ATOM	545	O	GLU	A	169	23.365	26.949	14.844	1.00	15.48	A
ATOM	546	N	ARG	A	170	23.349	27.268	12.615	1.00	14.29	A
ATOM	547	CA	ARG	A	170	24.149	26.077	12.363	1.00	13.93	A
ATOM	548	CB	ARG	A	170	24.206	25.757	10.867	1.00	15.66	A
ATOM	549	CG	ARG	A	170	25.057	24.536	10.535	1.00	20.09	A
ATOM	550	CD	ARG	A	170	24.452	23.251	11.095	1.00	23.76	A
ATOM	551	NE	ARG	A	170	23.147	22.970	10.502	1.00	28.96	A
ATOM	552	CZ	ARG	A	170	22.019	22.859	11.197	1.00	31.03	A
ATOM	553	NH1	ARG	A	170	22.031	23.000	12.514	1.00	33.04	A
ATOM	554	NH2	ARG	A	170	20.875	22.616	10.573	1.00	35.19	A
ATOM	555	C	ARG	A	170	25.557	26.301	12.899	1.00	13.95	A
ATOM	556	O	ARG	A	170	26.167	25.387	13.455	1.00	12.96	A
ATOM	557	N	LEU	A	171	26.070	27.518	12.736	1.00	12.17	A
ATOM	558	CA	LEU	A	171	27.407	27.839	13.233	1.00	11.76	A
ATOM	559	CB	LEU	A	171	27.796	29.269	12.854	1.00	12.30	A
ATOM	560	CG	LEU	A	171	27.693	29.625	11.371	1.00	11.31	A
ATOM	561	CD1	LEU	A	171	28.133	31.070	11.170	1.00	12.66	A
ATOM	562	CD2	LEU	A	171	28.552	28.677	10.546	1.00	12.20	A
ATOM	563	C	LEU	A	171	27.447	27.687	14.755	1.00	11.70	A
ATOM	564	O	LEU	A	171	28.425	27.190	15.311	1.00	11.76	A
ATOM	565	N	LEU	A	172	26.382	28.114	15.427	1.00	11.75	A
ATOM	566	CA	LEU	A	172	26.321	28.001	16.880	1.00	12.10	A
ATOM	567	CB	LEU	A	172	25.049	28.656	17.424	1.00	12.80	A
ATOM	568	CG	LEU	A	172	24.981	30.178	17.302	1.00	14.86	A
ATOM	569	CD1	LEU	A	172	23.659	30.671	17.874	1.00	16.13	A
ATOM	570	CD2	LEU	A	172	26.153	30.811	18.043	1.00	15.33	A
ATOM	571	C	LEU	A	172	26.379	26.546	17.324	1.00	12.23	A
ATOM	572	O	LEU	A	172	27.018	26.227	18.326	1.00	12.62	A
ATOM	573	N	ALA	A	173	25.712	25.665	16.580	1.00	12.72	A
ATOM	574	CA	ALA	A	173	25.713	24.245	16.919	1.00	13.14	A
ATOM	575	CB	ALA	A	173	24.720	23.486	16.041	1.00	11.87	A
ATOM	576	C	ALA	A	173	27.112	23.665	16.747	1.00	12.63	A
ATOM	577	O	ALA	A	173	27.578	22.894	17.581	1.00	11.33	A
ATOM	578	N	VAL	A	174	27.787	24.034	15.662	1.00	10.42	A
ATOM	579	CA	VAL	A	174	29.133	23.534	15.428	1.00	9.27	A
ATOM	580	CB	VAL	A	174	29.662	23.953	14.041	1.00	9.04	A
ATOM	581	CG1	VAL	A	174	31.093	23.458	13.861	1.00	8.42	A
ATOM	582	CG2	VAL	A	174	28.763	23.386	12.955	1.00	9.09	A
ATOM	583	C	VAL	A	174	30.075	24.073	16.499	1.00	10.17	A
ATOM	584	O	VAL	A	174	30.953	23.358	16.977	1.00	10.23	A
ATOM	585	N	ALA	A	175	29.886	25.335	16.877	1.00	9.90	A
ATOM	586	CA	ALA	A	175	30.725	25.951	17.897	1.00	10.67	A
ATOM	587	CB	ALA	A	175	30.316	27.407	18.108	1.00	11.94	A
ATOM	588	C	ALA	A	175	30.611	25.182	19.208	1.00	11.92	A
ATOM	589	O	ALA	A	175	31.616	24.883	19.847	1.00	11.33	A
ATOM	590	N	GLU	A	176	29.383	24.854	19.600	1.00	13.20	A
ATOM	591	CA	GLU	A	176	29.163	24.119	20.845	1.00	13.21	A
ATOM	592	CB	GLU	A	176	27.664	23.932	21.099	1.00	15.61	A
ATOM	593	CG	GLU	A	176	27.349	23.074	22.326	1.00	19.61	A
ATOM	594	CD	GLU	A	176	25.879	23.099	22.705	1.00	23.95	A
ATOM	595	OE1	GLU	A	176	25.027	23.172	21.795	1.00	25.62	A
ATOM	596	OE2	GLU	A	176	25.573	23.030	23.916	1.00	27.39	A
ATOM	597	C	GLU	A	176	29.854	22.762	20.793	1.00	12.78	A
ATOM	598	O	GLU	A	176	30.477	22.325	21.762	1.00	13.68	A
ATOM	599	N	ARG	A	177	29.740	22.099	19.650	1.00	11.89	A
ATOM	600	CA	ARG	A	177	30.360	20.798	19.454	1.00	11.86	A
ATOM	601	CB	ARG	A	177	30.078	20.329	18.026	1.00	10.78	A
ATOM	602	CG	ARG	A	177	30.928	19.176	17.542	1.00	11.79	A
ATOM	603	CD	ARG	A	177	30.643	18.947	16.070	1.00	12.75	A
ATOM	604	NE	ARG	A	177	31.478	17.900	15.497	1.00	14.37	A
ATOM	605	CZ	ARG	A	177	31.587	17.681	14.193	1.00	13.51	A
ATOM	606	NH1	ARG	A	177	30.915	18.440	13.337	1.00	13.86	A
ATOM	607	NH2	ARG	A	177	32.366	16.708	13.746	1.00	13.82	A

ATOM	608	C	ARG	A	177	31.869	20.852	19.701	1.00	12.81	A
ATOM	609	O	ARG	A	177	32.447	19.941	20.297	1.00	11.57	A
ATOM	610	N	TYR	A	178	32.510	21.924	19.243	1.00	12.95	A
ATOM	611	CA	TYR	A	178	33.952	22.068	19.406	1.00	12.76	A
ATOM	612	CB	TYR	A	178	34.540	22.714	18.146	1.00	13.24	A
ATOM	613	CG	TYR	A	178	34.686	21.722	17.018	1.00	12.79	A
ATOM	614	CD1	TYR	A	178	35.763	20.834	16.987	1.00	12.88	A
ATOM	615	CE1	TYR	A	178	35.890	19.891	15.971	1.00	14.50	A
ATOM	616	CD2	TYR	A	178	33.736	21.642	16.002	1.00	12.10	A
ATOM	617	CE2	TYR	A	178	33.853	20.700	14.980	1.00	13.48	A
ATOM	618	CZ	TYR	A	178	34.933	19.831	14.972	1.00	13.02	A
ATOM	619	OH	TYR	A	178	35.066	18.902	13.966	1.00	16.93	A
ATOM	620	C	TYR	A	178	34.387	22.826	20.657	1.00	13.57	A
ATOM	621	O	TYR	A	178	35.571	23.115	20.837	1.00	14.22	A
ATOM	622	N	GLY	A	179	33.427	23.140	21.522	1.00	14.01	A
ATOM	623	CA	GLY	A	179	33.742	23.841	22.755	1.00	14.86	A
ATOM	624	C	GLY	A	179	34.238	25.260	22.561	1.00	15.37	A
ATOM	625	O	GLY	A	179	35.016	25.769	23.368	1.00	16.81	A
ATOM	626	N	LEU	A	180	33.788	25.903	21.491	1.00	14.92	A
ATOM	627	CA	LEU	A	180	34.182	27.276	21.208	1.00	15.19	A
ATOM	628	CB	LEU	A	180	34.468	27.447	19.719	1.00	16.63	A
ATOM	629	CG	LEU	A	180	35.636	26.648	19.147	1.00	15.00	A
ATOM	630	CD1	LEU	A	180	35.705	26.872	17.641	1.00	17.63	A
ATOM	631	CD2	LEU	A	180	36.931	27.079	19.815	1.00	19.25	A
ATOM	632	C	LEU	A	180	33.066	28.229	21.611	1.00	16.56	A
ATOM	633	O	LEU	A	180	31.897	27.842	21.669	1.00	17.28	A
ATOM	634	N	SER	A	181	33.434	29.475	21.891	1.00	16.35	A
ATOM	635	CA	SER	A	181	32.463	30.497	22.261	1.00	16.39	A
ATOM	636	CB	SER	A	181	33.177	31.792	22.647	1.00	17.27	A
ATOM	637	OG	SER	A	181	32.259	32.871	22.715	1.00	18.74	A
ATOM	638	C	SER	A	181	31.556	30.764	21.067	1.00	16.14	A
ATOM	639	O	SER	A	181	32.029	31.173	20.009	1.00	15.41	A
ATOM	640	N	GLY	A	182	30.258	30.534	21.240	1.00	15.64	A
ATOM	641	CA	GLY	A	182	29.320	30.759	20.156	1.00	14.80	A
ATOM	642	C	GLY	A	182	29.312	32.209	19.708	1.00	14.74	A
ATOM	643	O	GLY	A	182	29.257	32.502	18.508	1.00	14.19	A
ATOM	644	N	SER	A	183	29.377	33.124	20.673	1.00	16.05	A
ATOM	645	CA	SER	A	183	29.377	34.549	20.365	1.00	17.71	A
ATOM	646	CB	SER	A	183	29.274	35.374	21.654	1.00	17.19	A
ATOM	647	OG	SER	A	183	30.314	35.052	22.557	1.00	21.78	A
ATOM	648	C	SER	A	183	30.626	34.942	19.579	1.00	16.35	A
ATOM	649	O	SER	A	183	30.534	35.682	18.595	1.00	16.95	A
ATOM	650	N	ASP	A	184	31.789	34.453	20.006	1.00	15.79	A
ATOM	651	CA	ASP	A	184	33.028	34.754	19.297	1.00	15.34	A
ATOM	652	CB	ASP	A	184	34.243	34.153	20.009	1.00	17.96	A
ATOM	653	CG	ASP	A	184	34.646	34.928	21.244	1.00	21.29	A
ATOM	654	OD1	ASP	A	184	34.198	36.082	21.401	1.00	22.54	A
ATOM	655	OD2	ASP	A	184	35.430	34.384	22.050	1.00	24.60	A
ATOM	656	C	ASP	A	184	32.966	34.183	17.884	1.00	14.07	A
ATOM	657	O	ASP	A	184	33.351	34.847	16.923	1.00	14.53	A
ATOM	658	N	VAL	A	185	32.485	32.948	17.762	1.00	12.60	A
ATOM	659	CA	VAL	A	185	32.393	32.309	16.451	1.00	10.90	A
ATOM	660	CB	VAL	A	185	31.812	30.875	16.565	1.00	10.19	A
ATOM	661	CG1	VAL	A	185	31.437	30.336	15.178	1.00	11.57	A
ATOM	662	CG2	VAL	A	185	32.854	29.957	17.206	1.00	11.80	A
ATOM	663	C	VAL	A	185	31.552	33.139	15.483	1.00	10.62	A
ATOM	664	O	VAL	A	185	31.947	33.347	14.336	1.00	11.96	A
ATOM	665	N	LEU	A	186	30.406	33.633	15.937	1.00	11.61	A
ATOM	666	CA	LEU	A	186	29.568	34.441	15.056	1.00	12.75	A
ATOM	667	CB	LEU	A	186	28.206	34.719	15.698	1.00	13.84	A
ATOM	668	CG	LEU	A	186	27.315	33.502	15.965	1.00	15.35	A
ATOM	669	CD1	LEU	A	186	25.951	33.981	16.429	1.00	17.79	A
ATOM	670	CD2	LEU	A	186	27.170	32.663	14.709	1.00	16.34	A
ATOM	671	C	LEU	A	186	30.246	35.761	14.698	1.00	12.81	A
ATOM	672	O	LEU	A	186	30.136	36.235	13.565	1.00	13.44	A
ATOM	673	N	ASP	A	187	30.938	36.362	15.659	1.00	12.21	A
ATOM	674	CA	ASP	A	187	31.619	37.627	15.394	1.00	14.99	A
ATOM	675	CB	ASP	A	187	32.163	38.255	16.678	1.00	16.78	A

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ATOM    676  CG  ASP A 187      31.074  38.721  17.619  1.00 20.35      A
ATOM    677  OD1 ASP A 187      29.988  39.116  17.147  1.00 21.97      A
ATOM    678  OD2 ASP A 187      31.324  38.706  18.843  1.00 25.56      A
ATOM    679  C   ASP A 187      32.791  37.436  14.440  1.00 15.26      A
ATOM    680  O   ASP A 187      33.259  38.400  13.830  1.00 15.23      A
ATOM    681  N   ASN A 188      33.270  36.200  14.322  1.00 13.87      A
ATOM    682  CA  ASN A 188      34.403  35.905  13.450  1.00 14.14      A
ATOM    683  CB  ASN A 188      35.368  34.942  14.135  1.00 14.82      A
ATOM    684  CG  ASN A 188      36.110  35.587  15.281  1.00 18.85      A
ATOM    685  OD1 ASN A 188      36.520  36.744  15.195  1.00 20.12      A
ATOM    686  ND2 ASN A 188      36.306  34.836  16.357  1.00 21.10      A
ATOM    687  C   ASN A 188      34.050  35.359  12.072  1.00 13.53      A
ATOM    688  O   ASN A 188      34.929  34.904  11.343  1.00 13.36      A
ATOM    689  N   VAL A 189      32.769  35.367  11.727  1.00 12.06      A
ATOM    690  CA  VAL A 189      32.357  34.924  10.402  1.00 10.87      A
ATOM    691  CB  VAL A 189      31.309  33.779  10.446  1.00  9.92      A
ATOM    692  CG1 VAL A 189      30.851  33.443   9.026  1.00  9.91      A
ATOM    693  CG2 VAL A 189      31.913  32.537  11.092  1.00 10.65      A
ATOM    694  C   VAL A 189      31.726  36.135   9.725  1.00 13.11      A
ATOM    695  O   VAL A 189      30.705  36.642  10.187  1.00 14.95      A
ATOM    696  N   ALA A 190      32.352  36.614   8.653  1.00 11.72      A
ATOM    697  CA  ALA A 190      31.825  37.753   7.905  1.00 11.20      A
ATOM    698  CB  ALA A 190      32.961  38.597   7.353  1.00 10.95      A
ATOM    699  C   ALA A 190      30.992  37.170   6.773  1.00 11.60      A
ATOM    700  O   ALA A 190      31.458  36.303   6.032  1.00 12.58      A
ATOM    701  N   TYR A 191      29.765  37.658   6.643  1.00  9.10      A
ATOM    702  CA  TYR A 191      28.829  37.157   5.646  1.00 11.15      A
ATOM    703  CB  TYR A 191      27.653  36.493   6.377  1.00 14.31      A
ATOM    704  CG  TYR A 191      26.381  36.329   5.573  1.00 16.33      A
ATOM    705  CD1 TYR A 191      26.292  35.384   4.550  1.00 18.03      A
ATOM    706  CE1 TYR A 191      25.116  35.219   3.819  1.00 21.10      A
ATOM    707  CD2 TYR A 191      25.259  37.110   5.846  1.00 19.21      A
ATOM    708  CE2 TYR A 191      24.077  36.955   5.120  1.00 21.77      A
ATOM    709  CZ  TYR A 191      24.012  36.007   4.110  1.00 22.07      A
ATOM    710  OH  TYR A 191      22.842  35.844   3.399  1.00 24.46      A
ATOM    711  C   TYR A 191      28.296  38.219   4.701  1.00  9.98      A
ATOM    712  O   TYR A 191      28.083  39.363   5.091  1.00 10.36      A
ATOM    713  N   ALA A 192      28.085  37.823   3.452  1.00  9.94      A
ATOM    714  CA  ALA A 192      27.527  38.718   2.452  1.00 10.77      A
ATOM    715  CB  ALA A 192      28.635  39.455   1.709  1.00 11.74      A
ATOM    716  C   ALA A 192      26.725  37.881   1.478  1.00 12.63      A
ATOM    717  O   ALA A 192      27.075  36.735   1.204  1.00 13.05      A
ATOM    718  N   ARG A 193      25.630  38.432    .974  1.00 14.15      A
ATOM    719  CA  ARG A 193      24.857  37.701   -.013  1.00 16.28      A
ATOM    720  CB  ARG A 193      23.381  37.591    .372  1.00 18.72      A
ATOM    721  CG  ARG A 193      22.590  36.823   -.680  1.00 18.20      A
ATOM    722  CD  ARG A 193      21.215  36.423   -.216  1.00 21.34      A
ATOM    723  NE  ARG A 193      20.500  35.721  -1.275  1.00 20.08      A
ATOM    724  CZ  ARG A 193      19.286  35.204  -1.138  1.00 21.29      A
ATOM    725  NH1 ARG A 193      18.647  35.307    .022  1.00 22.51      A
ATOM    726  NH2 ARG A 193      18.709  34.591  -2.161  1.00 20.69      A
ATOM    727  C   ARG A 193      24.997  38.467  -1.314  1.00 15.74      A
ATOM    728  O   ARG A 193      24.666  39.650  -1.380  1.00 17.52      A
ATOM    729  N   ALA A 194      25.518  37.798  -2.339  1.00 13.91      A
ATOM    730  CA  ALA A 194      25.706  38.422  -3.641  1.00 15.22      A
ATOM    731  CB  ALA A 194      26.674  37.593  -4.482  1.00 13.64      A
ATOM    732  C   ALA A 194      24.353  38.530  -4.333  1.00 15.34      A
ATOM    733  O   ALA A 194      23.612  37.550  -4.424  1.00 15.21      A
ATOM    734  N   PHE A 195      24.040  39.730  -4.811  1.00 16.95      A
ATOM    735  CA  PHE A 195      22.770  39.999  -5.478  1.00 19.87      A
ATOM    736  CB  PHE A 195      22.384  41.466  -5.268  1.00 19.91      A
ATOM    737  CG  PHE A 195      21.846  41.761  -3.894  1.00 22.04      A
ATOM    738  CD1 PHE A 195      22.553  41.386  -2.757  1.00 24.87      A
ATOM    739  CD2 PHE A 195      20.625  42.407  -3.737  1.00 22.22      A
ATOM    740  CE1 PHE A 195      22.051  41.648  -1.481  1.00 25.60      A
ATOM    741  CE2 PHE A 195      20.114  42.674  -2.466  1.00 22.41      A
ATOM    742  CZ  PHE A 195      20.829  42.293  -1.337  1.00 24.456     A
ATOM    743  C   PHE A 195      22.789  39.670  -6.967  1.00 19.68      A
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ATOM	744	O	PHE	A	195	21.758	39.329	-7.550	1.00	21.50	A
ATOM	745	N	ASN	A	196	23.963	39.779	-7.577	1.00	17.00	A
ATOM	746	CA	ASN	A	196	24.129	39.485	-8.996	1.00	18.09	A
ATOM	747	CB	ASN	A	196	23.633	40.658	-9.848	1.00	18.40	A
ATOM	748	CG	ASN	A	196	24.312	41.964	-9.495	1.00	19.85	A
ATOM	749	OD1	ASN	A	196	25.514	42.124	-9.689	1.00	20.52	A
ATOM	750	ND2	ASN	A	196	23.540	42.910	-8.966	1.00	22.23	A
ATOM	751	C	ASN	A	196	25.609	39.218	-9.253	1.00	16.35	A
ATOM	752	O	ASN	A	196	26.427	39.344	-8.344	1.00	14.96	A
ATOM	753	N	THR	A	197	25.959	38.858	-10.483	1.00	17.26	A
ATOM	754	CA	THR	A	197	27.354	38.557	-10.791	1.00	16.17	A
ATOM	755	CB	THR	A	197	27.494	37.932	-12.195	1.00	17.31	A
ATOM	756	OG1	THR	A	197	26.899	38.793	-13.171	1.00	20.03	A
ATOM	757	CG2	THR	A	197	26.813	36.571	-12.234	1.00	18.30	A
ATOM	758	C	THR	A	197	28.322	39.730	-10.654	1.00	16.37	A
ATOM	759	O	THR	A	197	29.496	39.525	-10.338	1.00	13.66	A
ATOM	760	N	ASP	A	198	27.857	40.956	-10.894	1.00	16.79	A
ATOM	761	CA	ASP	A	198	28.741	42.107	-10.742	1.00	18.01	A
ATOM	762	CB	ASP	A	198	28.095	43.394	-11.271	1.00	22.18	A
ATOM	763	CG	ASP	A	198	28.117	43.486	-12.786	1.00	26.46	A
ATOM	764	OD1	ASP	A	198	28.972	42.833	-13.420	1.00	29.30	A
ATOM	765	OD2	ASP	A	198	27.287	44.235	-13.341	1.00	31.93	A
ATOM	766	C	ASP	A	198	29.050	42.284	-9.259	1.00	17.29	A
ATOM	767	O	ASP	A	198	30.197	42.523	-8.874	1.00	17.00	A
ATOM	768	N	HIS	A	199	28.014	42.165	-8.432	1.00	15.89	A
ATOM	769	CA	HIS	A	199	28.163	42.310	-6.989	1.00	14.74	A
ATOM	770	CB	HIS	A	199	26.804	42.211	-6.296	1.00	14.97	A
ATOM	771	CG	HIS	A	199	26.862	42.446	-4.818	1.00	13.46	A
ATOM	772	CD2	HIS	A	199	27.658	43.249	-4.075	1.00	12.84	A
ATOM	773	ND1	HIS	A	199	26.015	41.818	-3.931	1.00	14.71	A
ATOM	774	CE1	HIS	A	199	26.290	42.223	-2.703	1.00	13.89	A
ATOM	775	NE2	HIS	A	199	27.281	43.092	-2.763	1.00	14.41	A
ATOM	776	C	HIS	A	199	29.075	41.211	-6.454	1.00	13.93	A
ATOM	777	O	HIS	A	199	29.907	41.454	-5.581	1.00	12.91	A
ATOM	778	N	GLN	A	200	28.902	40.005	-6.985	1.00	13.22	A
ATOM	779	CA	GLN	A	200	29.702	38.854	-6.573	1.00	12.96	A
ATOM	780	CB	GLN	A	200	29.331	37.642	-7.421	1.00	12.31	A
ATOM	781	CG	GLN	A	200	30.026	36.352	-7.013	1.00	13.47	A
ATOM	782	CD	GLN	A	200	29.566	35.175	-7.848	1.00	13.16	A
ATOM	783	OE1	GLN	A	200	28.375	35.028	-8.125	1.00	15.14	A
ATOM	784	NE2	GLN	A	200	30.504	34.321	-8.245	1.00	13.84	A
ATOM	785	C	GLN	A	200	31.191	39.147	-6.717	1.00	13.87	A
ATOM	786	O	GLN	A	200	31.994	38.816	-5.840	1.00	12.77	A
ATOM	787	N	THR	A	201	31.556	39.765	-7.834	1.00	11.64	A
ATOM	788	CA	THR	A	201	32.948	40.109	-8.086	1.00	12.73	A
ATOM	789	CB	THR	A	201	33.178	40.403	-9.593	1.00	11.84	A
ATOM	790	OG1	THR	A	201	33.216	39.168	-10.321	1.00	13.35	A
ATOM	791	CG2	THR	A	201	34.479	41.155	-9.803	1.00	14.26	A
ATOM	792	C	THR	A	201	33.377	41.313	-7.244	1.00	11.26	A
ATOM	793	O	THR	A	201	34.495	41.350	-6.727	1.00	11.94	A
ATOM	794	N	GLN	A	202	32.485	42.289	-7.092	1.00	12.98	A
ATOM	795	CA	GLN	A	202	32.803	43.477	-6.312	1.00	13.80	A
ATOM	796	CB	GLN	A	202	31.639	44.475	-6.360	1.00	17.53	A
ATOM	797	CG	GLN	A	202	32.024	45.875	-5.899	1.00	25.23	A
ATOM	798	CD	GLN	A	202	32.228	45.970	-4.400	1.00	28.15	A
ATOM	799	OE1	GLN	A	202	33.065	46.738	-3.922	1.00	32.69	A
ATOM	800	NE2	GLN	A	202	31.455	45.194	-3.647	1.00	29.89	A
ATOM	801	C	GLN	A	202	33.123	43.115	-4.863	1.00	12.44	A
ATOM	802	O	GLN	A	202	33.972	43.742	-4.235	1.00	13.52	A
ATOM	803	N	LEU	A	203	32.449	42.094	-4.342	1.00	12.46	A
ATOM	804	CA	LEU	A	203	32.672	41.655	-2.968	1.00	11.73	A
ATOM	805	CB	LEU	A	203	31.704	40.519	-2.608	1.00	12.52	A
ATOM	806	CG	LEU	A	203	30.257	40.950	-2.332	1.00	12.51	A
ATOM	807	CD1	LEU	A	203	29.347	39.739	-2.274	1.00	14.88	A
ATOM	808	CD2	LEU	A	203	30.204	41.722	-1.023	1.00	15.21	A
ATOM	809	C	LEU	A	203	34.115	41.215	-2.719	1.00	12.56	A
ATOM	810	O	LEU	A	203	34.605	41.288	-1.590	1.00	11.56	A
ATOM	811	N	LEU	A	204	34.801	40.768	-3.767	1.00	11.31	A

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ATOM    812  CA  LEU A 204      36.185  40.339  -3.611  1.00 11.87      A
ATOM    813  CB  LEU A 204      36.672  39.614  -4.865  1.00 11.53      A
ATOM    814  CG  LEU A 204      35.976  38.285  -5.169  1.00 12.00      A
ATOM    815  CD1 LEU A 204      36.753  37.566  -6.269  1.00 12.14      A
ATOM    816  CD2 LEU A 204      35.920  37.417  -3.913  1.00 12.53      A
ATOM    817  C   LEU A 204      37.109  41.513  -3.294  1.00 11.61      A
ATOM    818  O   LEU A 204      38.158  41.335  -2.679  1.00 11.18      A
ATOM    819  N   TYR A 205      36.730  42.712  -3.724  1.00 13.97      A
ATOM    820  CA  TYR A 205      37.544  43.883  -3.425  1.00 16.07      A
ATOM    821  CB  TYR A 205      37.097  45.073  -4.274  1.00 19.68      A
ATOM    822  CG  TYR A 205      37.769  45.087  -5.621  1.00 23.06      A
ATOM    823  CD1 TYR A 205      39.088  45.522  -5.752  1.00 26.38      A
ATOM    824  CE1 TYR A 205      39.742  45.482  -6.977  1.00 28.42      A
ATOM    825  CD2 TYR A 205      37.114  44.616  -6.755  1.00 24.97      A
ATOM    826  CE2 TYR A 205      37.760  44.569  -7.989  1.00 27.75      A
ATOM    827  CZ  TYR A 205      39.073  45.004  -8.091  1.00 29.20      A
ATOM    828  OH  TYR A 205      39.722  44.956  -9.304  1.00 32.07      A
ATOM    829  C   TYR A 205      37.415  44.192  -1.940  1.00 15.39      A
ATOM    830  O   TYR A 205      38.408  44.484  -1.268  1.00 14.26      A
ATOM    831  N   GLN A 206      36.191  44.113  -1.426  1.00 14.66      A
ATOM    832  CA  GLN A 206      35.957  44.355   -.007  1.00 14.18      A
ATOM    833  CB  GLN A 206      34.459  44.298    .310  1.00 16.50      A
ATOM    834  CG  GLN A 206      33.621  45.297   -.469  1.00 21.42      A
ATOM    835  CD  GLN A 206      32.151  45.230   -.103  1.00 24.13      A
ATOM    836  OE1 GLN A 206      31.282  45.253   -.975  1.00 26.96      A
ATOM    837  NE2 GLN A 206      31.863  45.156  1.193  1.00 26.12      A
ATOM    838  C   GLN A 206      36.682  43.262    .768  1.00 11.99      A
ATOM    839  O   GLN A 206      37.325  43.520  1.784  1.00 13.05      A
ATOM    840  N   ALA A 207      36.577  42.033    .276  1.00 11.37      A
ATOM    841  CA  ALA A 207      37.224  40.901    .924  1.00  9.55      A
ATOM    842  CB  ALA A 207      36.981  39.630   .112  1.00 11.15      A
ATOM    843  C   ALA A 207      38.726  41.137  1.086  1.00  9.68      A
ATOM    844  O   ALA A 207      39.286  40.901  2.154  1.00 10.32      A
ATOM    845  N   SER   208      39.370  41.607   .021   .50  8.91      AC1
ATOM    846  CA  SER   208      40.809  41.855   .055   .50  8.84      AC1
ATOM    847  CB  SER   208      41.319  42.271 -1.332   .50  8.15      AC1
ATOM    848  OG  SER   208      40.748  43.489 -1.778   .50  5.66      AC1
ATOM    849  C   SER   208      41.180  42.910  1.091   .50  8.91      AC1
ATOM    850  O   SER   208      42.186  42.773  1.787   .50  9.06      AC1
ATOM    851  N   ALA A 209      40.364  43.955  1.198  1.00  9.46      A
ATOM    852  CA  ALA A 209      40.613  45.020  2.163  1.00 10.03      A
ATOM    853  CB  ALA A 209      39.631  46.163  1.940  1.00 11.01      A
ATOM    854  C   ALA A 209      40.474  44.466  3.581  1.00 12.23      A
ATOM    855  O   ALA A 209      41.252  44.796  4.474  1.00 13.45      A
ATOM    856  N   MSE A 210      39.483  43.608  3.782  1.00 11.13      A
ATOM    857  CA  MSE A 210      39.263  43.015  5.093  1.00 11.31      A
ATOM    858  CB  MSE A 210      37.939  42.245  5.087  1.00 11.10      A
ATOM    859  CG  MSE A 210      36.738  43.163  4.929  1.00 12.90      A
ATOM    860  SE  MSE A 210      35.166  42.285  4.275  1.00 19.56      A
ATOM    861  CE  MSE A 210      34.748  41.258  5.846  1.00 18.08      A
ATOM    862  C   MSE A 210      40.416  42.100  5.502  1.00 10.40      A
ATOM    863  O   MSE A 210      40.816  42.075  6.667  1.00 11.49      A
ATOM    864  N   MSE A 211      40.959  41.361  4.538  1.00  9.79      A
ATOM    865  CA  MSE A 211      42.054  40.442  4.809  1.00  9.90      A
ATOM    866  CB  MSE A 211      42.246  39.502  3.622  1.00 11.35      A
ATOM    867  CG  MSE A 211      41.034  38.605  3.419  1.00 13.28      A
ATOM    868  SE  MSE A 211      41.249  37.350  1.970  1.00 19.97      A
ATOM    869  CE  MSE A 211      39.669  36.267  2.266  1.00 17.37      A
ATOM    870  C   MSE A 211      43.354  41.161  5.150  1.00 12.40      A
ATOM    871  O   MSE A 211      44.254  40.576  5.751  1.00 12.31      A
ATOM    872  N   VAL A 212      43.448  42.429  4.771  1.00 13.63      A
ATOM    873  CA  VAL A 212      44.633  43.219  5.092  1.00 16.42      A
ATOM    874  CB  VAL A 212      44.710  44.499  4.215  1.00 16.91      A
ATOM    875  CG1 VAL A 212      45.666  45.507  4.837  1.00 20.67      A
ATOM    876  CG2 VAL A 212      45.179  44.141  2.815  1.00 16.11      A
ATOM    877  C   VAL A 212      44.566  43.633  6.565  1.00 18.07      A
ATOM    878  O   VAL A 212      45.587  43.696  7.256  1.00 20.15      A
ATOM    879  N   GLU A 213      43.351  43.890  7.039  1.00 17.71      A
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ATOM	880	CA	GLU	A	213	43.111	44.333	8.412	1.00	19.16	A
ATOM	881	CB	GLU	A	213	41.801	45.127	8.470	1.00	21.15	A
ATOM	882	CG	GLU	A	213	41.862	46.502	7.823	1.00	24.58	A
ATOM	883	CD	GLU	A	213	40.552	47.263	7.955	1.00	28.91	A
ATOM	884	OE1	GLU	A	213	39.820	47.024	8.940	1.00	29.96	A
ATOM	885	OE2	GLU	A	213	40.257	48.111	7.085	1.00	30.33	A
ATOM	886	C	GLU	A	213	43.076	43.256	9.498	1.00	19.63	A
ATOM	887	O	GLU	A	213	43.546	43.486	10.614	1.00	18.83	A
ATOM	888	N	SER	A	214	42.509	42.093	9.184	1.00	18.76	A
ATOM	889	CA	SER	A	214	42.399	41.004	10.159	1.00	18.30	A
ATOM	890	CB	SER	A	214	40.945	40.857	10.626	1.00	20.42	A
ATOM	891	OG	SER	A	214	40.397	42.099	11.016	1.00	25.34	A
ATOM	892	C	SER	A	214	42.839	39.686	9.546	1.00	17.21	A
ATOM	893	O	SER	A	214	42.840	39.540	8.324	1.00	15.90	A
ATOM	894	N	ARG	A	215	43.190	38.719	10.391	1.00	16.03	A
ATOM	895	CA	ARG	A	215	43.612	37.419	9.891	1.00	14.50	A
ATOM	896	CB	ARG	A	215	44.521	36.686	10.885	1.00	17.55	A
ATOM	897	CG	ARG	A	215	44.837	35.257	10.414	1.00	20.04	A
ATOM	898	CD	ARG	A	215	45.692	34.456	11.384	1.00	25.67	A
ATOM	899	NE	ARG	A	215	45.705	33.035	11.032	1.00	28.44	A
ATOM	900	CZ	ARG	A	215	46.186	32.539	9.894	1.00	32.44	A
ATOM	901	NH1	ARG	A	215	46.710	33.342	8.977	1.00	33.60	A
ATOM	902	NH2	ARG	A	215	46.132	31.232	9.664	1.00	33.47	A
ATOM	903	C	ARG	A	215	42.444	36.502	9.568	1.00	13.33	A
ATOM	904	O	ARG	A	215	41.666	36.124	10.448	1.00	14.15	A
ATOM	905	N	TYR	A	216	42.337	36.148	8.294	1.00	12.11	A
ATOM	906	CA	TYR	A	216	41.309	35.235	7.826	1.00	10.66	A
ATOM	907	CB	TYR	A	216	40.597	35.796	6.600	1.00	11.82	A
ATOM	908	CG	TYR	A	216	39.502	36.761	6.941	1.00	11.74	A
ATOM	909	CD1	TYR	A	216	39.789	38.074	7.311	1.00	13.91	A
ATOM	910	CE1	TYR	A	216	38.773	38.950	7.670	1.00	14.14	A
ATOM	911	CD2	TYR	A	216	38.172	36.348	6.939	1.00	13.07	A
ATOM	912	CE2	TYR	A	216	37.157	37.209	7.296	1.00	13.62	A
ATOM	913	CZ	TYR	A	216	37.459	38.506	7.661	1.00	15.01	A
ATOM	914	OH	TYR	A	216	36.434	39.349	8.016	1.00	17.98	A
ATOM	915	C	TYR	A	216	41.996	33.942	7.435	1.00	10.55	A
ATOM	916	O	TYR	A	216	43.151	33.952	7.012	1.00	11.94	A
ATOM	917	N	ALA	A	217	41.288	32.829	7.572	1.00	8.82	A
ATOM	918	CA	ALA	A	217	41.849	31.538	7.200	1.00	8.08	A
ATOM	919	CB	ALA	A	217	41.849	30.599	8.403	1.00	10.40	A
ATOM	920	C	ALA	A	217	41.023	30.927	6.082	1.00	8.74	A
ATOM	921	O	ALA	A	217	41.492	30.030	5.380	1.00	9.17	A
ATOM	922	N	LEU	A	218	39.811	31.440	5.889	1.00	8.26	A
ATOM	923	CA	LEU	A	218	38.913	30.856	4.897	1.00	9.02	A
ATOM	924	CB	LEU	A	218	38.089	29.765	5.593	1.00	9.51	A
ATOM	925	CG	LEU	A	218	36.917	29.094	4.872	1.00	10.64	A
ATOM	926	CD1	LEU	A	218	37.450	28.079	3.870	1.00	11.06	A
ATOM	927	CD2	LEU	A	218	36.024	28.398	5.892	1.00	13.12	A
ATOM	928	C	LEU	A	218	37.946	31.799	4.184	1.00	7.66	A
ATOM	929	O	LEU	A	218	37.368	32.697	4.794	1.00	8.43	A
ATOM	930	N	LEU	A	219	37.778	31.571	2.885	1.00	8.37	A
ATOM	931	CA	LEU	A	219	36.821	32.322	2.078	1.00	7.10	A
ATOM	932	CB	LEU	A	219	37.507	33.171	1.000	1.00	9.27	A
ATOM	933	CG	LEU	A	219	36.542	33.707	-.075	1.00	10.99	A
ATOM	934	CD1	LEU	A	219	35.445	34.564	.560	1.00	13.35	A
ATOM	935	CD2	LEU	A	219	37.322	34.518	-1.101	1.00	12.85	A
ATOM	936	C	LEU	A	219	35.929	31.294	1.395	1.00	7.22	A
ATOM	937	O	LEU	A	219	36.412	30.419	.668	1.00	7.85	A
ATOM	938	N	ILE		220	34.627	31.412	1.626	.50	6.12	AC1
ATOM	939	CA	ILE		220	33.644	30.508	1.045	.50	5.48	AC1
ATOM	940	CB	ILE		220	32.706	29.953	2.131	.50	5.16	AC1
ATOM	941	CG2	ILE		220	31.606	29.110	1.492	.50	5.91	AC1
ATOM	942	CG1	ILE		220	33.509	29.143	3.150	.50	4.87	AC1
ATOM	943	CD1	ILE		220	32.776	28.924	4.455	.50	2.48	AC1
ATOM	944	C	ILE		220	32.785	31.247	.029	.50	5.49	AC1
ATOM	945	O	ILE		220	32.343	32.369	.281	.50	5.14	AC1
ATOM	946	N	VAL	A	221	32.555	30.616	-1.118	1.00	6.21	A
ATOM	947	CA	VAL	A	221	31.713	31.202	-2.158	1.00	6.05	A

ATOM	948	CB	VAL	A	221	32.479	31.630	-3.418	1.00	8.43	A
ATOM	949	CG1	VAL	A	221	31.489	32.232	-4.424	1.00	11.56	A
ATOM	950	CG2	VAL	A	221	33.545	32.652	-3.065	1.00	9.56	A
ATOM	951	C	VAL	A	221	30.747	30.083	-2.525	1.00	9.19	A
ATOM	952	O	VAL	A	221	31.097	29.156	-3.257	1.00	9.66	A
ATOM	953	N	ASP	A	222	29.530	30.182	-2.001	1.00	8.99	A
ATOM	954	CA	ASP	A	222	28.488	29.178	-2.208	1.00	10.19	A
ATOM	955	CB	ASP	A	222	28.237	28.482	-.859	1.00	12.30	A
ATOM	956	CG	ASP	A	222	27.093	27.492	-.899	1.00	13.65	A
ATOM	957	OD1	ASP	A	222	26.893	26.851	-1.945	1.00	14.21	A
ATOM	958	OD2	ASP	A	222	26.407	27.343	.138	1.00	17.00	A
ATOM	959	C	ASP	A	222	27.218	29.870	-2.712	1.00	10.73	A
ATOM	960	O	ASP	A	222	26.485	30.447	-1.914	1.00	11.04	A
ATOM	961	N	SER	A	223	26.926	29.815	-4.014	1.00	11.76	A
ATOM	962	CA	SER	A	223	27.693	29.127	-5.053	1.00	11.53	A
ATOM	963	CB	SER	A	223	26.717	28.320	-5.922	1.00	13.99	A
ATOM	964	OG	SER	A	223	27.250	28.040	-7.204	1.00	15.91	A
ATOM	965	C	SER	A	223	28.470	30.107	-5.937	1.00	12.18	A
ATOM	966	O	SER	A	223	28.063	31.256	-6.113	1.00	12.29	A
ATOM	967	N	ALA	A	224	29.578	29.649	-6.509	1.00	11.55	A
ATOM	968	CA	ALA	A	224	30.389	30.505	-7.365	1.00	12.08	A
ATOM	969	CB	ALA	A	224	31.815	29.960	-7.447	1.00	12.08	A
ATOM	970	C	ALA	A	224	29.812	30.646	-8.771	1.00	12.99	A
ATOM	971	O	ALA	A	224	30.159	31.578	-9.495	1.00	13.90	A
ATOM	972	N	THR	A	225	28.916	29.741	-9.150	1.00	14.01	A
ATOM	973	CA	THR	A	225	28.355	29.777	-10.497	1.00	15.06	A
ATOM	974	CB	THR	A	225	28.715	28.492	-11.251	1.00	15.67	A
ATOM	975	OG1	THR	A	225	28.169	27.367	-10.550	1.00	18.32	A
ATOM	976	CG2	THR	A	225	30.227	28.341	-11.350	1.00	17.70	A
ATOM	977	C	THR	A	225	26.844	29.966	-10.621	1.00	16.24	A
ATOM	978	O	THR	A	225	26.353	30.310	-11.696	1.00	16.22	A
ATOM	979	N	ALA	A	226	26.111	29.742	-9.536	1.00	15.40	A
ATOM	980	CA	ALA	A	226	24.655	29.863	-9.569	1.00	17.16	A
ATOM	981	CB	ALA	A	226	24.087	29.724	-8.157	1.00	17.20	A
ATOM	982	C	ALA	A	226	24.121	31.139	-10.218	1.00	18.11	A
ATOM	983	O	ALA	A	226	23.215	31.080	-11.050	1.00	19.76	A
ATOM	984	N	LEU	A	227	24.677	32.289	-9.849	1.00	17.52	A
ATOM	985	CA	LEU	A	227	24.207	33.558	-10.396	1.00	17.98	A
ATOM	986	CB	LEU	A	227	24.802	34.726	-9.603	1.00	18.01	A
ATOM	987	CG	LEU	A	227	24.397	34.787	-8.123	1.00	18.20	A
ATOM	988	CD1	LEU	A	227	24.978	36.043	-7.489	1.00	19.48	A
ATOM	989	CD2	LEU	A	227	22.876	34.783	-7.992	1.00	21.19	A
ATOM	990	C	LEU	A	227	24.481	33.740	-11.890	1.00	18.80	A
ATOM	991	O	LEU	A	227	23.895	34.616	-12.530	1.00	18.94	A
ATOM	992	N	TYR	A	228	25.360	32.911	-12.443	1.00	18.50	A
ATOM	993	CA	TYR	A	228	25.693	32.986	-13.863	1.00	21.58	A
ATOM	994	CB	TYR	A	228	27.107	32.450	-14.099	1.00	17.41	A
ATOM	995	CG	TYR	A	228	28.196	33.411	-13.689	1.00	14.92	A
ATOM	996	CD1	TYR	A	228	28.626	34.417	-14.554	1.00	12.76	A
ATOM	997	CE1	TYR	A	228	29.620	35.314	-14.179	1.00	13.80	A
ATOM	998	CD2	TYR	A	228	28.789	33.328	-12.430	1.00	13.04	A
ATOM	999	CE2	TYR	A	228	29.785	34.224	-12.044	1.00	12.87	A
ATOM	1000	CZ	TYR	A	228	30.196	35.211	-12.920	1.00	12.36	A
ATOM	1001	OH	TYR	A	228	31.182	36.091	-12.551	1.00	14.32	A
ATOM	1002	C	TYR	A	228	24.699	32.205	-14.717	1.00	25.16	A
ATOM	1003	O	TYR	A	228	24.694	32.327	-15.942	1.00	27.01	A
ATOM	1004	N	ARG	A	229	23.857	31.409	-14.066	1.00	28.73	A
ATOM	1005	CA	ARG	A	229	22.861	30.608	-14.770	1.00	34.06	A
ATOM	1006	CB	ARG	A	229	22.862	29.173	-14.233	1.00	37.97	A
ATOM	1007	CG	ARG	A	229	21.948	28.221	-14.994	1.00	45.76	A
ATOM	1008	CD	ARG	A	229	22.082	26.795	-14.476	1.00	50.57	A
ATOM	1009	NE	ARG	A	229	21.591	26.658	-13.107	1.00	56.15	A
ATOM	1010	CZ	ARG	A	229	20.304	26.628	-12.771	1.00	58.13	A
ATOM	1011	NH1	ARG	A	229	19.366	26.723	-13.705	1.00	59.34	A
ATOM	1012	NH2	ARG	A	229	19.955	26.504	-11.498	1.00	59.67	A
ATOM	1013	C	ARG	A	229	21.469	31.210	-14.619	1.00	35.05	A
ATOM	1014	O	ARG	A	229	21.162	32.242	-15.216	1.00	37.10	A
ATOM	1015	N	GLU	A	237	26.455	36.730	-25.203	1.00	45.75	A

ATOM	1016	CA	GLU	A	237	25.871	36.676	-23.870	1.00	45.26	A
ATOM	1017	CB	GLU	A	237	24.361	36.455	-23.965	1.00	47.65	A
ATOM	1018	CG	GLU	A	237	23.661	36.374	-22.618	1.00	51.11	A
ATOM	1019	CD	GLU	A	237	24.004	37.545	-21.718	1.00	52.82	A
ATOM	1020	OE1	GLU	A	237	23.878	38.701	-22.172	1.00	54.95	A
ATOM	1021	OE2	GLU	A	237	24.397	37.309	-20.555	1.00	53.95	A
ATOM	1022	C	GLU	A	237	26.505	35.558	-23.052	1.00	43.96	A
ATOM	1023	O	GLU	A	237	27.098	35.803	-22.001	1.00	43.47	A
ATOM	1024	N	LEU	A	238	26.371	34.329	-23.541	1.00	41.51	A
ATOM	1025	CA	LEU	A	238	26.937	33.170	-22.866	1.00	39.97	A
ATOM	1026	CB	LEU	A	238	26.619	31.896	-23.650	1.00	41.06	A
ATOM	1027	CG	LEU	A	238	27.342	30.621	-23.203	1.00	42.05	A
ATOM	1028	CD1	LEU	A	238	27.008	30.309	-21.751	1.00	42.90	A
ATOM	1029	CD2	LEU	A	238	26.935	29.469	-24.107	1.00	43.61	A
ATOM	1030	C	LEU	A	238	28.447	33.318	-22.725	1.00	38.07	A
ATOM	1031	O	LEU	A	238	29.005	33.095	-21.651	1.00	36.76	A
ATOM	1032	N	SER	A	239	29.105	33.693	-23.818	1.00	35.69	A
ATOM	1033	CA	SER	A	239	30.552	33.870	-23.813	1.00	33.46	A
ATOM	1034	CB	SER	A	239	31.055	34.167	-25.227	1.00	34.80	A
ATOM	1035	OG	SER	A	239	30.508	35.377	-25.721	1.00	37.47	A
ATOM	1036	C	SER	A	239	30.947	35.005	-22.875	1.00	31.86	A
ATOM	1037	O	SER	A	239	32.013	34.973	-22.260	1.00	30.28	A
ATOM	1038	N	ALA	A	240	30.082	36.008	-22.769	1.00	29.26	A
ATOM	1039	CA	ALA	A	240	30.344	37.146	-21.897	1.00	27.57	A
ATOM	1040	CB	ALA	A	240	29.276	38.212	-22.091	1.00	28.86	A
ATOM	1041	C	ALA	A	240	30.359	36.676	-20.446	1.00	26.33	A
ATOM	1042	O	ALA	A	240	31.229	37.065	-19.665	1.00	24.83	A
ATOM	1043	N	ARG	A	241	29.391	35.837	-20.095	1.00	24.47	A
ATOM	1044	CA	ARG	A	241	29.298	35.308	-18.741	1.00	24.64	A
ATOM	1045	CB	ARG	A	241	27.986	34.545	-18.545	1.00	26.26	A
ATOM	1046	CG	ARG	A	241	26.748	35.415	-18.618	1.00	30.40	A
ATOM	1047	CD	ARG	A	241	25.509	34.636	-18.222	1.00	32.71	A
ATOM	1048	NE	ARG	A	241	24.309	35.459	-18.327	1.00	37.68	A
ATOM	1049	CZ	ARG	A	241	23.094	35.063	-17.964	1.00	40.61	A
ATOM	1050	NH1	ARG	A	241	22.910	33.848	-17.465	1.00	42.19	A
ATOM	1051	NH2	ARG	A	241	22.061	35.883	-18.104	1.00	41.34	A
ATOM	1052	C	ARG	A	241	30.467	34.381	-18.436	1.00	23.05	A
ATOM	1053	O	ARG	A	241	30.986	34.376	-17.321	1.00	21.52	A
ATOM	1054	N	GLN	A	242	30.882	33.597	-19.427	1.00	21.32	A
ATOM	1055	CA	GLN	A	242	31.991	32.675	-19.227	1.00	22.07	A
ATOM	1056	CB	GLN	A	242	32.152	31.754	-20.442	1.00	26.14	A
ATOM	1057	CG	GLN	A	242	31.006	30.759	-20.591	1.00	32.63	A
ATOM	1058	CD	GLN	A	242	31.207	29.788	-21.737	1.00	37.09	A
ATOM	1059	OE1	GLN	A	242	31.310	30.188	-22.897	1.00	39.23	A
ATOM	1060	NE2	GLN	A	242	31.259	28.499	-21.415	1.00	39.89	A
ATOM	1061	C	GLN	A	242	33.291	33.417	-18.946	1.00	19.58	A
ATOM	1062	O	GLN	A	242	34.074	32.992	-18.098	1.00	17.88	A
ATOM	1063	N	MSE	A	243	33.519	34.521	-19.652	1.00	18.13	A
ATOM	1064	CA	MSE	A	243	34.729	35.313	-19.444	1.00	18.31	A
ATOM	1065	CB	MSE	A	243	34.868	36.397	-20.519	1.00	20.88	A
ATOM	1066	CG	MSE	A	243	35.243	35.872	-21.895	1.00	24.97	A
ATOM	1067	SE	MSE	A	243	35.643	37.308	-23.133	1.00	31.39	A
ATOM	1068	CE	MSE	A	243	33.856	37.603	-23.805	1.00	31.87	A
ATOM	1069	C	MSE	A	243	34.701	35.976	-18.073	1.00	17.43	A
ATOM	1070	O	MSE	A	243	35.715	36.041	-17.384	1.00	15.93	A
ATOM	1071	N	HIS	A	244	33.532	36.473	-17.684	1.00	15.35	A
ATOM	1072	CA	HIS	A	244	33.382	37.135	-16.396	1.00	14.53	A
ATOM	1073	CB	HIS	A	244	31.975	37.732	-16.286	1.00	16.88	A
ATOM	1074	CG	HIS	A	244	31.813	38.698	-15.155	1.00	18.28	A
ATOM	1075	CD2	HIS	A	244	31.863	40.050	-15.125	1.00	17.28	A
ATOM	1076	ND1	HIS	A	244	31.585	38.294	-13.857	1.00	17.51	A
ATOM	1077	CE1	HIS	A	244	31.502	39.355	-13.076	1.00	17.03	A
ATOM	1078	NE2	HIS	A	244	31.667	40.435	-13.820	1.00	18.85	A
ATOM	1079	C	HIS	A	244	33.645	36.141	-15.264	1.00	13.42	A
ATOM	1080	O	HIS	A	244	34.323	36.466	-14.290	1.00	11.85	A
ATOM	1081	N	LEU	A	245	33.111	34.931	-15.400	1.00	12.32	A
ATOM	1082	CA	LEU	A	245	33.313	33.894	-14.393	1.00	11.41	A
ATOM	1083	CB	LEU	A	245	32.459	32.664	-14.716	1.00	11.93	A

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ATOM   1084  CG  LEU A 245      32.704  31.410 -13.869  1.00 12.45      A
ATOM   1085  CD1 LEU A 245      32.472  31.715 -12.389  1.00 12.44      A
ATOM   1086  CD2 LEU A 245      31.778  30.300 -14.339  1.00 13.60      A
ATOM   1087  C   LEU A 245      34.790  33.504 -14.341  1.00 11.45      A
ATOM   1088  O   LEU A 245      35.363  33.358 -13.263  1.00 11.37      A
ATOM   1089  N   ALA A 246      35.411  33.344 -15.506  1.00 11.75      A
ATOM   1090  CA  ALA A 246      36.822  32.976 -15.558  1.00 11.29      A
ATOM   1091  CB  ALA A 246      37.298  32.895 -17.007  1.00 11.67      A
ATOM   1092  C   ALA A 246      37.655  33.998 -14.791  1.00 11.07      A
ATOM   1093  O   ALA A 246      38.552  33.638 -14.032  1.00 10.62      A
ATOM   1094  N   ARG A 247      37.344  35.274 -14.985  1.00 11.10      A
ATOM   1095  CA  ARG A 247      38.064  36.337 -14.300  1.00 12.88      A
ATOM   1096  CB  ARG A 247      37.572  37.702 -14.774  1.00 17.27      A
ATOM   1097  CG  ARG A 247      38.347  38.868 -14.189  1.00 25.65      A
ATOM   1098  CD  ARG A 247      39.732  38.971 -14.804  1.00 32.96      A
ATOM   1099  NE  ARG A 247      40.475  40.118 -14.287  1.00 39.20      A
ATOM   1100  CZ  ARG A 247      41.244  40.089 -13.204  1.00 41.96      A
ATOM   1101  NH1 ARG A 247      41.387  38.965 -12.512  1.00 42.95      A
ATOM   1102  NH2 ARG A 247      41.862  41.192 -12.807  1.00 43.69      A
ATOM   1103  C   ARG A 247      37.841  36.204 -12.795  1.00 11.48      A
ATOM   1104  O   ARG A 247      38.779  36.316 -12.005  1.00 11.35      A
ATOM   1105  N   PHE A 248      36.591  35.971 -12.406  1.00  9.96      A
ATOM   1106  CA  PHE A 248      36.257  35.809 -10.993  1.00  8.76      A
ATOM   1107  CB  PHE A 248      34.775  35.465 -10.831  1.00  8.82      A
ATOM   1108  CG  PHE A 248      34.360  35.228  -9.402  1.00  8.05      A
ATOM   1109  CD1 PHE A 248      34.228  36.293  -8.515  1.00  9.83      A
ATOM   1110  CD2 PHE A 248      34.111  33.937  -8.942  1.00  9.86      A
ATOM   1111  CE1 PHE A 248      33.853  36.076  -7.186  1.00  8.69      A
ATOM   1112  CE2 PHE A 248      33.735  33.708  -7.617  1.00  9.42      A
ATOM   1113  CZ  PHE A 248      33.607  34.781  -6.738  1.00  8.27      A
ATOM   1114  C   PHE A 248      37.098  34.698 -10.367  1.00  8.86      A
ATOM   1115  O   PHE A 248      37.636  34.861  -9.274  1.00  9.14      A
ATOM   1116  N   LEU A 249      37.205  33.567 -11.059  1.00  9.66      A
ATOM   1117  CA  LEU A 249      37.971  32.435 -10.542  1.00  9.31      A
ATOM   1118  CB  LEU A 249      37.736  31.195 -11.415  1.00  8.82      A
ATOM   1119  CG  LEU A 249      36.283  30.708 -11.405  1.00 13.09      A
ATOM   1120  CD1 LEU A 249      36.127  29.567 -12.393  1.00 13.38      A
ATOM   1121  CD2 LEU A 249      35.888  30.265  -9.996  1.00 12.31      A
ATOM   1122  C   LEU A 249      39.462  32.744 -10.429  1.00 10.28      A
ATOM   1123  O   LEU A 249      40.126  32.268  -9.505  1.00  9.43      A
ATOM   1124  N   ARG A 250      39.999  33.536 -11.355  1.00  9.79      A
ATOM   1125  CA  ARG A 250      41.410  33.897 -11.270  1.00  9.23      A
ATOM   1126  CB  ARG A 250      41.899  34.549 -12.573  1.00 10.09      A
ATOM   1127  CG  ARG A 250      41.905  33.591 -13.770  1.00 10.89      A
ATOM   1128  CD  ARG A 250      42.923  34.015 -14.832  1.00 12.35      A
ATOM   1129  NE  ARG A 250      42.692  35.372 -15.318  1.00 14.15      A
ATOM   1130  CZ  ARG A 250      41.768  35.713 -16.213  1.00 12.84      A
ATOM   1131  NH1 ARG A 250      40.968  34.793 -16.744  1.00 12.74      A
ATOM   1132  NH2 ARG A 250      41.642  36.985 -16.573  1.00 13.32      A
ATOM   1133  C   ARG A 250      41.617  34.851 -10.087  1.00  9.42      A
ATOM   1134  O   ARG A 250      42.674  34.852  -9.461  1.00 10.80      A
ATOM   1135  N   MSE A 251      40.603  35.660  -9.786  1.00  8.99      A
ATOM   1136  CA  MSE A 251      40.693  36.585  -8.664  1.00  7.90      A
ATOM   1137  CB  MSE A 251      39.503  37.546  -8.655  1.00 10.28      A
ATOM   1138  CG  MSE A 251      39.546  38.555  -9.787  1.00 10.58      A
ATOM   1139  SE  MSE A 251      37.927  39.597  -9.882  1.00 19.52      A
ATOM   1140  CE  MSE A 251      38.253  40.781  -8.392  1.00 16.71      A
ATOM   1141  C   MSE A 251      40.728  35.785  -7.368  1.00  8.49      A
ATOM   1142  O   MSE A 251      41.453  36.134  -6.441  1.00  8.06      A
ATOM   1143  N   LEU A 252      39.946  34.708  -7.306  1.00  8.09      A
ATOM   1144  CA  LEU A 252      39.936  33.873  -6.109  1.00  8.04      A
ATOM   1145  CB  LEU A 252      38.891  32.757  -6.222  1.00  8.32      A
ATOM   1146  CG  LEU A 252      37.411  33.159  -6.168  1.00  8.66      A
ATOM   1147  CD1 LEU A 252      36.544  31.914  -6.288  1.00  9.22      A
ATOM   1148  CD2 LEU A 252      37.104  33.889  -4.867  1.00  9.32      A
ATOM   1149  C   LEU A 252      41.314  33.262  -5.899  1.00  9.42      A
ATOM   1150  O   LEU A 252      41.800  33.177  -4.771  1.00  9.61      A
ATOM   1151  N   LEU A 253      41.944  32.834  -6.990  1.00  9.24      A
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ATOM	1152	CA	LEU	A	253	43.271	32.239	-6.910	1.00	11.62	A
ATOM	1153	CB	LEU	A	253	43.696	31.706	-8.282	1.00	13.39	A
ATOM	1154	CG	LEU	A	253	45.049	30.990	-8.331	1.00	17.43	A
ATOM	1155	CD1	LEU	A	253	45.023	29.793	-7.394	1.00	20.44	A
ATOM	1156	CD2	LEU	A	253	45.351	30.550	-9.761	1.00	20.02	A
ATOM	1157	C	LEU	A	253	44.276	33.279	-6.413	1.00	11.13	A
ATOM	1158	O	LEU	A	253	45.169	32.960	-5.627	1.00	11.41	A
ATOM	1159	N	ARG	A	254	44.129	34.520	-6.871	1.00	11.69	A
ATOM	1160	CA	ARG	A	254	45.022	35.600	-6.450	1.00	13.18	A
ATOM	1161	CB	ARG	A	254	44.700	36.888	-7.219	1.00	15.17	A
ATOM	1162	CG	ARG	A	254	45.686	38.045	-7.004	1.00	21.07	A
ATOM	1163	CD	ARG	A	254	47.047	37.763	-7.645	1.00	26.19	A
ATOM	1164	NE	ARG	A	254	47.962	37.064	-6.746	1.00	35.54	A
ATOM	1165	CZ	ARG	A	254	48.623	37.648	-5.751	1.00	38.24	A
ATOM	1166	NH1	ARG	A	254	48.474	38.948	-5.527	1.00	41.13	A
ATOM	1167	NH2	ARG	A	254	49.434	36.934	-4.979	1.00	39.76	A
ATOM	1168	C	ARG	A	254	44.860	35.835	-4.943	1.00	12.40	A
ATOM	1169	O	ARG	A	254	45.843	36.054	-4.233	1.00	13.42	A
ATOM	1170	N	LEU	A	255	43.623	35.788	-4.452	1.00	11.26	A
ATOM	1171	CA	LEU	A	255	43.383	35.977	-3.023	1.00	11.62	A
ATOM	1172	CB	LEU	A	255	41.879	36.014	-2.717	1.00	12.84	A
ATOM	1173	CG	LEU	A	255	41.140	37.298	-3.105	1.00	17.32	A
ATOM	1174	CD1	LEU	A	255	39.664	37.180	-2.748	1.00	15.50	A
ATOM	1175	CD2	LEU	A	255	41.770	38.479	-2.372	1.00	16.31	A
ATOM	1176	C	LEU	A	255	44.043	34.852	-2.226	1.00	12.01	A
ATOM	1177	O	LEU	A	255	44.672	35.103	-1.197	1.00	10.55	A
ATOM	1178	N	ALA	A	256	43.901	33.616	-2.701	1.00	12.67	A
ATOM	1179	CA	ALA	A	256	44.507	32.474	-2.017	1.00	14.15	A
ATOM	1180	CB	ALA	A	256	44.103	31.165	-2.701	1.00	12.71	A
ATOM	1181	C	ALA	A	256	46.029	32.614	-1.996	1.00	15.50	A
ATOM	1182	O	ALA	A	256	46.671	32.310	-.988	1.00	17.69	A
ATOM	1183	N	ASP	A	257	46.601	33.077	-3.106	1.00	16.20	A
ATOM	1184	CA	ASP	A	257	48.050	33.266	-3.209	1.00	18.87	A
ATOM	1185	CB	ASP	A	257	48.465	33.654	-4.633	1.00	20.67	A
ATOM	1186	CG	ASP	A	257	48.336	32.520	-5.621	1.00	25.45	A
ATOM	1187	OD1	ASP	A	257	48.382	31.348	-5.202	1.00	26.70	A
ATOM	1188	OD2	ASP	A	257	48.210	32.812	-6.830	1.00	27.63	A
ATOM	1189	C	ASP	A	257	48.536	34.380	-2.296	1.00	18.97	A
ATOM	1190	O	ASP	A	257	49.505	34.227	-1.552	1.00	19.55	A
ATOM	1191	N	GLU	A	258	47.852	35.512	-2.374	1.00	15.45	A
ATOM	1192	CA	GLU	A	258	48.214	36.695	-1.613	1.00	15.96	A
ATOM	1193	CB	GLU	A	258	47.364	37.874	-2.090	1.00	15.35	A
ATOM	1194	CG	GLU	A	258	47.812	39.233	-1.579	1.00	19.78	A
ATOM	1195	CD	GLU	A	258	49.205	39.596	-2.052	1.00	21.75	A
ATOM	1196	OE1	GLU	A	258	49.551	39.254	-3.204	1.00	24.81	A
ATOM	1197	OE2	GLU	A	258	49.949	40.232	-1.277	1.00	24.19	A
ATOM	1198	C	GLU	A	258	48.098	36.580	-.100	1.00	15.06	A
ATOM	1199	O	GLU	A	258	49.035	36.918	.627	1.00	14.21	A
ATOM	1200	N	PHE	A	259	46.953	36.092	.365	1.00	12.81	A
ATOM	1201	CA	PHE	A	259	46.678	36.003	1.794	1.00	12.40	A
ATOM	1202	CB	PHE	A	259	45.275	36.549	2.048	1.00	14.06	A
ATOM	1203	CG	PHE	A	259	45.103	37.973	1.612	1.00	13.57	A
ATOM	1204	CD1	PHE	A	259	45.752	39.002	2.290	1.00	15.40	A
ATOM	1205	CD2	PHE	A	259	44.322	38.288	.505	1.00	13.21	A
ATOM	1206	CE1	PHE	A	259	45.625	40.326	1.872	1.00	14.07	A
ATOM	1207	CE2	PHE	A	259	44.188	39.610	.078	1.00	13.61	A
ATOM	1208	CZ	PHE	A	259	44.842	40.631	.763	1.00	15.29	A
ATOM	1209	C	PHE	A	259	46.828	34.642	2.461	1.00	13.00	A
ATOM	1210	O	PHE	A	259	46.724	34.539	3.684	1.00	14.38	A
ATOM	1211	N	GLY	A	260	47.068	33.604	1.668	1.00	12.99	A
ATOM	1212	CA	GLY	A	260	47.242	32.276	2.227	1.00	13.13	A
ATOM	1213	C	GLY	A	260	45.980	31.705	2.844	1.00	14.85	A
ATOM	1214	O	GLY	A	260	46.039	30.916	3.785	1.00	17.57	A
ATOM	1215	N	VAL	A	261	44.832	32.120	2.330	1.00	12.38	A
ATOM	1216	CA	VAL	A	261	43.568	31.615	2.843	1.00	11.17	A
ATOM	1217	CB	VAL	A	261	42.446	32.672	2.766	1.00	12.70	A
ATOM	1218	CG1	VAL	A	261	42.764	33.841	3.681	1.00	13.51	A
ATOM	1219	CG2	VAL	A	261	42.274	33.140	1.334	1.00	13.33	A

ATOM	1220	C	VAL	A	261	43.118	30.429	2.021	1.00	10.55	A
ATOM	1221	O	VAL	A	261	43.524	30.265	.871	1.00	11.12	A
ATOM	1222	N	ALA	A	262	42.285	29.594	2.623	1.00	8.95	A
ATOM	1223	CA	ALA	A	262	41.727	28.464	1.911	1.00	7.48	A
ATOM	1224	CB	ALA	A	262	41.299	27.378	2.886	1.00	8.32	A
ATOM	1225	C	ALA	A	262	40.508	29.059	1.224	1.00	8.31	A
ATOM	1226	O	ALA	A	262	39.759	29.815	1.842	1.00	11.69	A
ATOM	1227	N	VAL	A	263	40.322	28.746	-.053	1.00	6.91	A
ATOM	1228	CA	VAL	A	263	39.160	29.236	-.781	1.00	8.79	A
ATOM	1229	CB	VAL	A	263	39.563	29.988	-2.064	1.00	6.94	A
ATOM	1230	CG1	VAL	A	263	38.314	30.359	-2.868	1.00	9.46	A
ATOM	1231	CG2	VAL	A	263	40.349	31.238	-1.698	1.00	9.49	A
ATOM	1232	C	VAL	A	263	38.330	28.020	-1.150	1.00	7.77	A
ATOM	1233	O	VAL	A	263	38.807	27.124	-1.842	1.00	10.31	A
ATOM	1234	N	VAL	A	264	37.094	27.984	-.664	1.00	8.77	A
ATOM	1235	CA	VAL	A	264	36.196	26.870	-.933	1.00	8.22	A
ATOM	1236	CB	VAL	A	264	35.721	26.217	.381	1.00	8.51	A
ATOM	1237	CG1	VAL	A	264	34.704	25.114	.082	1.00	10.31	A
ATOM	1238	CG2	VAL	A	264	36.912	25.668	1.148	1.00	9.45	A
ATOM	1239	C	VAL	A	264	34.984	27.389	-1.686	1.00	9.72	A
ATOM	1240	O	VAL	A	264	34.284	28.280	-1.205	1.00	11.71	A
ATOM	1241	N	ILE	A	265	34.738	26.837	-2.868	1.00	10.40	A
ATOM	1242	CA	ILE	A	265	33.600	27.263	-3.660	1.00	10.29	A
ATOM	1243	CB	ILE	A	265	34.047	27.971	-4.957	1.00	10.14	A
ATOM	1244	CG2	ILE	A	265	35.016	29.101	-4.621	1.00	11.21	A
ATOM	1245	CG1	ILE	A	265	34.708	26.966	-5.907	1.00	12.27	A
ATOM	1246	CD1	ILE	A	265	35.143	27.565	-7.238	1.00	13.03	A
ATOM	1247	C	ILE	A	265	32.748	26.063	-4.034	1.00	10.17	A
ATOM	1248	O	ILE	A	265	33.236	24.935	-4.084	1.00	9.91	A
ATOM	1249	N	THR	A	266	31.470	26.305	-4.282	1.00	8.88	A
ATOM	1250	CA	THR	A	266	30.584	25.225	-4.676	1.00	9.58	A
ATOM	1251	CB	THR	A	266	29.349	25.134	-3.760	1.00	10.99	A
ATOM	1252	OG1	THR	A	266	28.518	26.287	-3.941	1.00	12.11	A
ATOM	1253	CG2	THR	A	266	29.785	25.052	-2.301	1.00	12.65	A
ATOM	1254	C	THR	A	266	30.161	25.483	-6.112	1.00	11.50	A
ATOM	1255	O	THR	A	266	30.132	26.628	-6.565	1.00	12.79	A
ATOM	1256	N	ASN	A	267	29.850	24.410	-6.828	1.00	12.20	A
ATOM	1257	CA	ASN	A	267	29.465	24.504	-8.227	1.00	13.60	A
ATOM	1258	CB	ASN	A	267	30.686	24.223	-9.103	1.00	14.59	A
ATOM	1259	CG	ASN	A	267	30.539	24.763	-10.510	1.00	17.75	A
ATOM	1260	OD1	ASN	A	267	29.429	24.953	-11.008	1.00	19.43	A
ATOM	1261	ND2	ASN	A	267	31.667	25.002	-11.166	1.00	17.66	A
ATOM	1262	C	ASN	A	267	28.391	23.458	-8.494	1.00	15.70	A
ATOM	1263	O	ASN	A	267	28.267	22.495	-7.738	1.00	15.21	A
ATOM	1264	N	ALA	A	293	40.359	24.063	-14.750	1.00	25.75	A
ATOM	1265	CA	ALA	A	293	40.748	24.289	-13.361	1.00	26.09	A
ATOM	1266	CB	ALA	A	293	40.228	23.156	-12.482	1.00	26.24	A
ATOM	1267	C	ALA	A	293	42.263	24.395	-13.226	1.00	26.19	A
ATOM	1268	O	ALA	A	293	43.008	23.745	-13.960	1.00	26.65	A
ATOM	1269	N	HIS	A	294	42.712	25.216	-12.283	1.00	24.21	A
ATOM	1270	CA	HIS	A	294	44.140	25.393	-12.051	1.00	23.37	A
ATOM	1271	CB	HIS	A	294	44.377	26.568	-11.098	1.00	23.08	A
ATOM	1272	CG	HIS	A	294	45.820	26.933	-10.933	1.00	25.13	A
ATOM	1273	CD2	HIS	A	294	46.623	27.742	-11.665	1.00	25.75	A
ATOM	1274	ND1	HIS	A	294	46.605	26.429	-9.919	1.00	24.49	A
ATOM	1275	CE1	HIS	A	294	47.831	26.914	-10.032	1.00	26.77	A
ATOM	1276	NE2	HIS	A	294	47.867	27.712	-11.084	1.00	26.73	A
ATOM	1277	C	HIS	A	294	44.713	24.110	-11.463	1.00	21.69	A
ATOM	1278	O	HIS	A	294	43.996	23.323	-10.841	1.00	20.98	A
ATOM	1279	N	ALA	A	295	46.006	23.897	-11.672	1.00	20.58	A
ATOM	1280	CA	ALA	A	295	46.677	22.704	-11.173	1.00	20.25	A
ATOM	1281	CB	ALA	A	295	48.154	22.749	-11.553	1.00	20.07	A
ATOM	1282	C	ALA	A	295	46.534	22.525	-9.662	1.00	19.38	A
ATOM	1283	O	ALA	A	295	46.484	21.397	-9.170	1.00	20.16	A
ATOM	1284	N	SER	A	296	46.451	23.632	-8.930	1.00	18.12	A
ATOM	1285	CA	SER	A	296	46.341	23.574	-7.472	1.00	17.16	A
ATOM	1286	CB	SER	A	296	46.902	24.858	-6.853	1.00	17.73	A
ATOM	1287	OG	SER	A	296	46.143	25.993	-7.244	1.00	17.47	A

ATOM	1288	C	SER	A	296	44.929	23.347	-6.943	1.00	18.00	A
ATOM	1289	O	SER	A	296	44.744	23.083	-5.755	1.00	17.02	A
ATOM	1290	N	THR	A	297	43.934	23.438	-7.816	1.00	15.86	A
ATOM	1291	CA	THR	A	297	42.552	23.259	-7.393	1.00	16.19	A
ATOM	1292	CB	THR	A	297	41.580	23.837	-8.446	1.00	16.61	A
ATOM	1293	OG1	THR	A	297	41.795	25.249	-8.558	1.00	19.45	A
ATOM	1294	CG2	THR	A	297	40.130	23.589	-8.042	1.00	18.10	A
ATOM	1295	C	THR	A	297	42.186	21.804	-7.121	1.00	16.88	A
ATOM	1296	O	THR	A	297	42.511	20.910	-7.899	1.00	19.37	A
ATOM	1297	N	THR	A	298	41.522	21.579	-5.993	1.00	14.80	A
ATOM	1298	CA	THR	A	298	41.072	20.248	-5.609	1.00	14.89	A
ATOM	1299	CB	THR	A	298	41.282	19.988	-4.103	1.00	16.40	A
ATOM	1300	OG1	THR	A	298	42.680	19.966	-3.812	1.00	18.58	A
ATOM	1301	CG2	THR	A	298	40.672	18.650	-3.697	1.00	18.79	A
ATOM	1302	C	THR	A	298	39.581	20.203	-5.890	1.00	13.32	A
ATOM	1303	O	THR	A	298	38.838	21.043	-5.398	1.00	12.51	A
ATOM	1304	N	ARG	A	299	39.149	19.232	-6.688	1.00	13.14	A
ATOM	1305	CA	ARG	A	299	37.735	19.094	-7.007	1.00	13.42	A
ATOM	1306	CB	ARG	A	299	37.543	18.923	-8.513	1.00	14.70	A
ATOM	1307	CG	ARG	A	299	37.595	20.223	-9.282	1.00	15.90	A
ATOM	1308	CD	ARG	A	299	37.341	19.992	-10.756	1.00	18.69	A
ATOM	1309	NE	ARG	A	299	37.088	21.244	-11.455	1.00	22.79	A
ATOM	1310	CZ	ARG	A	299	36.981	21.349	-12.773	1.00	23.75	A
ATOM	1311	NH1	ARG	A	299	37.111	20.271	-13.535	1.00	25.24	A
ATOM	1312	NH2	ARG	A	299	36.738	22.528	-13.327	1.00	24.88	A
ATOM	1313	C	ARG	A	299	37.101	17.919	-6.276	1.00	13.27	A
ATOM	1314	O	ARG	A	299	37.580	16.785	-6.365	1.00	16.01	A
ATOM	1315	N	LEU	A	300	36.024	18.201	-5.550	1.00	11.42	A
ATOM	1316	CA	LEU	A	300	35.302	17.181	-4.799	1.00	12.66	A
ATOM	1317	CB	LEU	A	300	35.158	17.594	-3.333	1.00	14.16	A
ATOM	1318	CG	LEU	A	300	36.415	18.043	-2.589	1.00	15.24	A
ATOM	1319	CD1	LEU	A	300	36.058	18.364	-1.142	1.00	15.73	A
ATOM	1320	CD2	LEU	A	300	37.469	16.963	-2.654	1.00	17.90	A
ATOM	1321	C	LEU	A	300	33.913	17.004	-5.391	1.00	13.73	A
ATOM	1322	O	LEU	A	300	33.200	17.981	-5.615	1.00	14.00	A
ATOM	1323	N	TYR	A	301	33.531	15.756	-5.649	1.00	13.54	A
ATOM	1324	CA	TYR	A	301	32.213	15.463	-6.197	1.00	13.49	A
ATOM	1325	CB	TYR	A	301	32.336	14.587	-7.446	1.00	15.65	A
ATOM	1326	CG	TYR	A	301	33.051	15.291	-8.577	1.00	17.58	A
ATOM	1327	CD1	TYR	A	301	34.443	15.368	-8.606	1.00	18.47	A
ATOM	1328	CE1	TYR	A	301	35.105	16.079	-9.602	1.00	19.95	A
ATOM	1329	CD2	TYR	A	301	32.332	15.945	-9.581	1.00	18.30	A
ATOM	1330	CE2	TYR	A	301	32.985	16.661	-10.583	1.00	20.78	A
ATOM	1331	CZ	TYR	A	301	34.371	16.725	-10.584	1.00	21.42	A
ATOM	1332	OH	TYR	A	301	35.025	17.440	-11.563	1.00	24.94	A
ATOM	1333	C	TYR	A	301	31.390	14.768	-5.122	1.00	13.26	A
ATOM	1334	O	TYR	A	301	31.678	13.634	-4.741	1.00	14.37	A
ATOM	1335	N	LEU	A	302	30.369	15.465	-4.633	1.00	11.70	A
ATOM	1336	CA	LEU	A	302	29.518	14.945	-3.570	1.00	12.66	A
ATOM	1337	CB	LEU	A	302	29.176	16.067	-2.584	1.00	13.35	A
ATOM	1338	CG	LEU	A	302	30.341	16.918	-2.075	1.00	14.08	A
ATOM	1339	CD1	LEU	A	302	29.806	18.031	-1.184	1.00	16.90	A
ATOM	1340	CD2	LEU	A	302	31.327	16.046	-1.317	1.00	14.36	A
ATOM	1341	C	LEU	A	302	28.221	14.332	-4.081	1.00	14.19	A
ATOM	1342	O	LEU	A	302	27.629	14.816	-5.046	1.00	15.47	A
ATOM	1343	N	ARG	A	303	27.783	13.264	-3.427	1.00	14.19	A
ATOM	1344	CA	ARG	A	303	26.531	12.624	-3.796	1.00	16.12	A
ATOM	1345	CB	ARG	A	303	26.757	11.496	-4.807	1.00	16.82	A
ATOM	1346	CG	ARG	A	303	27.559	10.303	-4.318	1.00	18.49	A
ATOM	1347	CD	ARG	A	303	27.532	9.215	-5.390	1.00	20.58	A
ATOM	1348	NE	ARG	A	303	28.155	7.963	-4.968	1.00	22.33	A
ATOM	1349	CZ	ARG	A	303	29.466	7.745	-4.928	1.00	24.00	A
ATOM	1350	NH1	ARG	A	303	30.318	8.698	-5.286	1.00	24.08	A
ATOM	1351	NH2	ARG	A	303	29.926	6.561	-4.541	1.00	24.43	A
ATOM	1352	C	ARG	A	303	25.846	12.099	-2.543	1.00	17.08	A
ATOM	1353	O	ARG	A	303	26.469	11.966	-1.485	1.00	15.73	A
ATOM	1354	N	LYS	A	304	24.556	11.810	-2.659	1.00	16.79	A
ATOM	1355	CA	LYS	A	304	23.812	11.334	-1.511	1.00	17.94	A

ATOM	1356	CB	LYS	A	304	22.314	11.601	-1.690	1.00	18.58	A
ATOM	1357	CG	LYS	A	304	21.506	11.138	-.488	1.00	22.70	A
ATOM	1358	CD	LYS	A	304	20.282	11.987	-.235	1.00	24.03	A
ATOM	1359	CE	LYS	A	304	19.806	11.807	1.199	1.00	21.77	A
ATOM	1360	NZ	LYS	A	304	19.638	10.368	1.563	1.00	19.38	A
ATOM	1361	C	LYS	A	304	24.025	9.868	-1.172	1.00	16.85	A
ATOM	1362	O	LYS	A	304	24.151	9.015	-2.055	1.00	18.41	A
ATOM	1363	N	GLY	A	305	24.089	9.604	.128	1.00	16.74	A
ATOM	1364	CA	GLY	A	305	24.237	8.254	.637	1.00	16.44	A
ATOM	1365	C	GLY	A	305	22.957	7.994	1.404	1.00	16.49	A
ATOM	1366	O	GLY	A	305	22.066	8.843	1.414	1.00	16.52	A
ATOM	1367	N	ARG	A	306	22.838	6.844	2.057	1.00	17.03	A
ATOM	1368	CA	ARG	A	306	21.614	6.569	2.798	1.00	18.22	A
ATOM	1369	CB	ARG	A	306	21.575	5.110	3.261	1.00	21.45	A
ATOM	1370	CG	ARG	A	306	20.253	4.741	3.913	1.00	27.33	A
ATOM	1371	CD	ARG	A	306	20.090	3.243	4.113	1.00	32.41	A
ATOM	1372	NE	ARG	A	306	21.051	2.699	5.067	1.00	36.11	A
ATOM	1373	CZ	ARG	A	306	20.914	1.520	5.662	1.00	37.74	A
ATOM	1374	NH1	ARG	A	306	19.853	.768	5.399	1.00	39.22	A
ATOM	1375	NH2	ARG	A	306	21.831	1.092	6.520	1.00	39.30	A
ATOM	1376	C	ARG	A	306	21.448	7.493	4.002	1.00	16.95	A
ATOM	1377	O	ARG	A	306	22.409	7.795	4.710	1.00	16.27	A
ATOM	1378	N	GLY	A	307	20.220	7.954	4.221	1.00	16.74	A
ATOM	1379	CA	GLY	A	307	19.946	8.824	5.350	1.00	14.78	A
ATOM	1380	C	GLY	A	307	20.798	10.080	5.393	1.00	16.48	A
ATOM	1381	O	GLY	A	307	20.848	10.843	4.426	1.00	15.11	A
ATOM	1382	N	GLU	A	308	21.476	10.289	6.519	1.00	16.48	A
ATOM	1383	CA	GLU	A	308	22.318	11.467	6.694	1.00	17.56	A
ATOM	1384	CB	GLU	A	308	22.399	11.838	8.182	1.00	19.01	A
ATOM	1385	CG	GLU	A	308	23.297	10.947	9.053	1.00	21.25	A
ATOM	1386	CD	GLU	A	308	22.828	9.501	9.145	1.00	24.06	A
ATOM	1387	OE1	GLU	A	308	21.610	9.266	9.285	1.00	23.79	A
ATOM	1388	OE2	GLU	A	308	23.686	8.595	9.095	1.00	26.02	A
ATOM	1389	C	GLU	A	308	23.726	11.301	6.132	1.00	16.66	A
ATOM	1390	O	GLU	A	308	24.532	12.235	6.185	1.00	15.98	A
ATOM	1391	N	THR	A	309	24.032	10.127	5.586	1.00	14.19	A
ATOM	1392	CA	THR	A	309	25.367	9.899	5.044	1.00	15.36	A
ATOM	1393	CB	THR	A	309	25.741	8.396	5.038	1.00	16.75	A
ATOM	1394	OG1	THR	A	309	24.944	7.694	4.077	1.00	17.63	A
ATOM	1395	CG2	THR	A	309	25.515	7.794	6.416	1.00	17.50	A
ATOM	1396	C	THR	A	309	25.507	10.461	3.637	1.00	14.74	A
ATOM	1397	O	THR	A	309	24.535	10.565	2.886	1.00	14.98	A
ATOM	1398	N	ARG	A	310	26.730	10.843	3.296	1.00	14.85	A
ATOM	1399	CA	ARG	A	310	27.027	11.410	1.989	1.00	14.16	A
ATOM	1400	CB	ARG	A	310	27.110	12.938	2.092	1.00	13.55	A
ATOM	1401	CG	ARG	A	310	25.824	13.620	2.565	1.00	14.48	A
ATOM	1402	CD	ARG	A	310	24.745	13.562	1.493	1.00	14.76	A
ATOM	1403	NE	ARG	A	310	23.552	14.340	1.830	1.00	15.70	A
ATOM	1404	CZ	ARG	A	310	22.574	13.926	2.632	1.00	16.49	A
ATOM	1405	NH1	ARG	A	310	22.634	12.730	3.199	1.00	14.99	A
ATOM	1406	NH2	ARG	A	310	21.523	14.708	2.854	1.00	15.34	A
ATOM	1407	C	ARG	A	310	28.362	10.846	1.532	1.00	13.62	A
ATOM	1408	O	ARG	A	310	29.150	10.355	2.343	1.00	14.37	A
ATOM	1409	N	ILE	A	311	28.619	10.911	.234	1.00	13.83	A
ATOM	1410	CA	ILE	A	311	29.871	10.404	-.297	1.00	15.05	A
ATOM	1411	CB	ILE	A	311	29.633	9.181	-1.206	1.00	17.49	A
ATOM	1412	CG2	ILE	A	311	30.958	8.671	-1.751	1.00	19.53	A
ATOM	1413	CG1	ILE	A	311	28.929	8.079	-.412	1.00	21.16	A
ATOM	1414	CD1	ILE	A	311	28.447	6.931	-1.269	1.00	24.48	A
ATOM	1415	C	ILE	A	311	30.599	11.477	-1.095	1.00	14.37	A
ATOM	1416	O	ILE	A	311	29.989	12.222	-1.866	1.00	14.03	A
ATOM	1417	N	CYS	A	312	31.907	11.560	-.884	1.00	13.85	A
ATOM	1418	CA	CYS	A	312	32.741	12.519	-1.588	1.00	13.35	A
ATOM	1419	CB	CYS	A	312	33.516	13.393	-.597	1.00	13.04	A
ATOM	1420	SG	CYS	A	312	34.710	14.505	-1.391	1.00	16.96	A
ATOM	1421	C	CYS	A	312	33.718	11.728	-2.440	1.00	14.32	A
ATOM	1422	O	CYS	A	312	34.361	10.793	-1.956	1.00	14.42	A
ATOM	1423	N	LYS	A	313	33.825	12.097	-3.710	1.00	14.16	A

ATOM	1424	CA	LYS	A	313	34.733	11.408	-4.610	1.00	15.69	A
ATOM	1425	CB	LYS	A	313	33.940	10.672	-5.693	1.00	18.29	A
ATOM	1426	CG	LYS	A	313	34.806	9.870	-6.650	1.00	21.66	A
ATOM	1427	CD	LYS	A	313	33.953	9.085	-7.636	1.00	27.84	A
ATOM	1428	CE	LYS	A	313	34.818	8.203	-8.525	1.00	31.20	A
ATOM	1429	NZ	LYS	A	313	34.006	7.412	-9.494	1.00	36.03	A
ATOM	1430	C	LYS	A	313	35.692	12.396	-5.258	1.00	16.66	A
ATOM	1431	O	LYS	A	313	35.300	13.510	-5.610	1.00	15.05	A
ATOM	1432	N	ILE	A	314	36.950	11.985	-5.391	1.00	17.72	A
ATOM	1433	CA	ILE	A	314	37.977	12.812	-6.016	1.00	22.21	A
ATOM	1434	CB	ILE	A	314	39.083	13.192	-5.016	1.00	22.48	A
ATOM	1435	CG2	ILE	A	314	40.135	14.053	-5.708	1.00	26.30	A
ATOM	1436	CG1	ILE	A	314	38.472	13.959	-3.843	1.00	21.65	A
ATOM	1437	CD1	ILE	A	314	39.476	14.366	-2.786	1.00	26.01	A
ATOM	1438	C	ILE	A	314	38.580	12.015	-7.169	1.00	26.09	A
ATOM	1439	O	ILE	A	314	38.628	10.785	-7.119	1.00	24.64	A
ATOM	1440	N	TYR	A	315	39.047	12.718	-8.197	1.00	31.43	A
ATOM	1441	CA	TYR	A	315	39.607	12.073	-9.383	1.00	37.29	A
ATOM	1442	CB	TYR	A	315	38.827	12.518	-10.616	1.00	37.68	A
ATOM	1443	CG	TYR	A	315	37.426	11.976	-10.689	1.00	38.88	A
ATOM	1444	CD1	TYR	A	315	37.179	10.702	-11.197	1.00	39.92	A
ATOM	1445	CE1	TYR	A	315	35.887	10.198	-11.275	1.00	39.85	A
ATOM	1446	CD2	TYR	A	315	36.342	12.736	-10.255	1.00	39.19	A
ATOM	1447	CE2	TYR	A	315	35.046	12.242	-10.325	1.00	39.96	A
ATOM	1448	CZ	TYR	A	315	34.825	10.971	-10.839	1.00	40.03	A
ATOM	1449	OH	TYR	A	315	33.547	10.474	-10.922	1.00	41.58	A
ATOM	1450	C	TYR	A	315	41.089	12.288	-9.656	1.00	41.54	A
ATOM	1451	O	TYR	A	315	41.827	12.818	-8.823	1.00	42.77	A
ATOM	1452	N	ASP	A	316	41.488	11.867	-10.857	1.00	45.11	A
ATOM	1453	CA	ASP	A	316	42.856	11.955	-11.364	1.00	48.76	A
ATOM	1454	CB	ASP	A	316	42.913	12.906	-12.562	1.00	51.10	A
ATOM	1455	CG	ASP	A	316	41.986	12.483	-13.685	1.00	53.20	A
ATOM	1456	OD1	ASP	A	316	41.864	11.263	-13.929	1.00	54.29	A
ATOM	1457	OD2	ASP	A	316	41.387	13.369	-14.331	1.00	55.12	A
ATOM	1458	C	ASP	A	316	43.901	12.364	-10.339	1.00	50.29	A
ATOM	1459	O	ASP	A	316	44.235	13.541	-10.202	1.00	50.40	A
ATOM	1460	N	SER	A	317	44.419	11.370	-9.628	1.00	51.63	A
ATOM	1461	CA	SER	A	317	45.433	11.596	-8.611	1.00	53.06	A
ATOM	1462	CB	SER	A	317	44.829	11.406	-7.217	1.00	53.24	A
ATOM	1463	OG	SER	A	317	43.646	12.170	-7.060	1.00	53.77	A
ATOM	1464	C	SER	A	317	46.563	10.596	-8.817	1.00	53.83	A
ATOM	1465	O	SER	A	317	46.346	9.385	-8.752	1.00	54.39	A
ATOM	1466	N	PRO	A	318	47.786	11.088	-9.079	1.00	54.06	A
ATOM	1467	CD	PRO	A	318	48.160	12.498	-9.289	1.00	54.37	A
ATOM	1468	CA	PRO	A	318	48.940	10.210	-9.291	1.00	53.91	A
ATOM	1469	CB	PRO	A	318	50.110	11.185	-9.282	1.00	54.17	A
ATOM	1470	CG	PRO	A	318	49.520	12.377	-9.956	1.00	54.74	A
ATOM	1471	C	PRO	A	318	49.057	9.138	-8.213	1.00	53.87	A
ATOM	1472	O	PRO	A	318	49.799	8.167	-8.365	1.00	54.39	A
ATOM	1473	N	CYS	A	319	48.320	9.321	-7.123	1.00	53.04	A
ATOM	1474	CA	CYS	A	319	48.323	8.365	-6.025	1.00	52.44	A
ATOM	1475	CB	CYS	A	319	48.105	9.089	-4.694	1.00	52.58	A
ATOM	1476	SG	CYS	A	319	49.423	10.257	-4.264	1.00	52.30	A
ATOM	1477	C	CYS	A	319	47.226	7.326	-6.247	1.00	52.16	A
ATOM	1478	O	CYS	A	319	47.417	6.143	-5.975	1.00	52.41	A
ATOM	1479	N	LEU	A	320	46.079	7.776	-6.749	1.00	51.37	A
ATOM	1480	CA	LEU	A	320	44.950	6.890	-7.020	1.00	50.25	A
ATOM	1481	CB	LEU	A	320	44.162	6.617	-5.735	1.00	51.58	A
ATOM	1482	CG	LEU	A	320	44.850	5.852	-4.600	1.00	52.61	A
ATOM	1483	CD1	LEU	A	320	43.919	5.791	-3.401	1.00	53.53	A
ATOM	1484	CD2	LEU	A	320	45.219	4.449	-5.062	1.00	53.34	A
ATOM	1485	C	LEU	A	320	44.024	7.519	-8.057	1.00	48.37	A
ATOM	1486	O	LEU	A	320	43.617	8.673	-7.917	1.00	48.51	A
ATOM	1487	N	PRO	A	321	43.681	6.769	-9.117	1.00	46.71	A
ATOM	1488	CD	PRO	A	321	44.099	5.390	-9.425	1.00	46.46	A
ATOM	1489	CA	PRO	A	321	42.795	7.290	-10.162	1.00	44.43	A
ATOM	1490	CB	PRO	A	321	42.474	6.047	-10.984	1.00	45.46	A
ATOM	1491	CG	PRO	A	321	43.749	5.270	-10.895	1.00	46.59	A

ATOM	1492	C	PRO	A	321	41.545	7.927	-9.562	1.00	41.95	A
ATOM	1493	O	PRO	A	321	41.167	9.042	-9.924	1.00	40.86	A
ATOM	1494	N	GLU	A	322	40.911	7.205	-8.644	1.00	39.09	A
ATOM	1495	CA	GLU	A	322	39.708	7.686	-7.978	1.00	36.24	A
ATOM	1496	CB	GLU	A	322	38.455	7.113	-8.646	1.00	39.05	A
ATOM	1497	CG	GLU	A	322	38.497	7.091	-10.165	1.00	43.79	A
ATOM	1498	CD	GLU	A	322	37.226	6.524	-10.770	1.00	46.15	A
ATOM	1499	OE1	GLU	A	322	36.680	5.555	-10.200	1.00	47.26	A
ATOM	1500	OE2	GLU	A	322	36.779	7.036	-11.818	1.00	48.33	A
ATOM	1501	C	GLU	A	322	39.744	7.232	-6.526	1.00	32.58	A
ATOM	1502	O	GLU	A	322	40.264	6.161	-6.213	1.00	31.65	A
ATOM	1503	N	ALA	A	323	39.197	8.054	-5.641	1.00	26.73	A
ATOM	1504	CA	ALA	A	323	39.151	7.722	-4.227	1.00	23.49	A
ATOM	1505	CB	ALA	A	323	40.367	8.285	-3.509	1.00	24.09	A
ATOM	1506	C	ALA	A	323	37.874	8.311	-3.655	1.00	21.23	A
ATOM	1507	O	ALA	A	323	37.432	9.382	-4.074	1.00	18.44	A
ATOM	1508	N	GLU	A	324	37.274	7.606	-2.706	1.00	20.46	A
ATOM	1509	CA	GLU	A	324	36.043	8.077	-2.100	1.00	21.25	A
ATOM	1510	CB	GLU	A	324	34.849	7.280	-2.624	1.00	23.33	A
ATOM	1511	CG	GLU	A	324	34.651	7.327	-4.124	1.00	27.34	A
ATOM	1512	CD	GLU	A	324	33.426	6.543	-4.550	1.00	29.02	A
ATOM	1513	OE1	GLU	A	324	33.318	5.362	-4.158	1.00	31.71	A
ATOM	1514	OE2	GLU	A	324	32.576	7.101	-5.272	1.00	30.39	A
ATOM	1515	C	GLU	A	324	36.074	7.951	-.589	1.00	20.52	A
ATOM	1516	O	GLU	A	324	36.831	7.158	-.029	1.00	21.51	A
ATOM	1517	N	ALA	A	325	35.237	8.746	.061	1.00	18.38	A
ATOM	1518	CA	ALA	A	325	35.120	8.719	1.505	1.00	18.27	A
ATOM	1519	CB	ALA	A	325	36.072	9.727	2.140	1.00	18.87	A
ATOM	1520	C	ALA	A	325	33.684	9.064	1.855	1.00	17.32	A
ATOM	1521	O	ALA	A	325	33.044	9.869	1.178	1.00	16.37	A
ATOM	1522	N	MSE		326	33.175	8.440	2.910	.51	16.14	AC1
ATOM	1523	CA	MSE		326	31.814	8.690	3.353	.51	15.49	AC1
ATOM	1524	CB	MSE		326	31.127	7.370	3.722	.51	16.90	AC1
ATOM	1525	CG	MSE		326	29.621	7.477	3.913	.51	17.28	AC1
ATOM	1526	SE	MSE		326	28.788	5.774	4.333	.51	21.71	AC1
ATOM	1527	CE	MSE		326	29.498	4.732	2.874	.51	24.72	AC1
ATOM	1528	C	MSE		326	31.863	9.603	4.571	.51	15.12	AC1
ATOM	1529	O	MSE		326	32.823	9.569	5.341	.51	16.04	AC1
ATOM	1530	N	PHE	A	327	30.837	10.432	4.728	1.00	14.66	A
ATOM	1531	CA	PHE	A	327	30.746	11.333	5.859	1.00	13.34	A
ATOM	1532	CB	PHE	A	327	31.439	12.686	5.582	1.00	14.23	A
ATOM	1533	CG	PHE	A	327	30.856	13.476	4.437	1.00	12.58	A
ATOM	1534	CD1	PHE	A	327	31.180	13.169	3.119	1.00	13.45	A
ATOM	1535	CD2	PHE	A	327	30.024	14.568	4.685	1.00	14.05	A
ATOM	1536	CE1	PHE	A	327	30.689	13.942	2.060	1.00	13.50	A
ATOM	1537	CE2	PHE	A	327	29.527	15.347	3.638	1.00	13.64	A
ATOM	1538	CZ	PHE	A	327	29.863	15.033	2.321	1.00	13.36	A
ATOM	1539	C	PHE	A	327	29.267	11.509	6.158	1.00	13.91	A
ATOM	1540	O	PHE	A	327	28.416	10.945	5.466	1.00	13.73	A
ATOM	1541	N	ALA	A	328	28.952	12.254	7.205	1.00	13.81	A
ATOM	1542	CA	ALA	A	328	27.560	12.464	7.558	1.00	13.68	A
ATOM	1543	CB	ALA	A	328	27.187	11.586	8.744	1.00	15.04	A
ATOM	1544	C	ALA	A	328	27.306	13.919	7.893	1.00	14.38	A
ATOM	1545	O	ALA	A	328	28.210	14.631	8.326	1.00	14.71	A
ATOM	1546	N	ILE	A	329	26.077	14.365	7.668	1.00	14.86	A
ATOM	1547	CA	ILE	A	329	25.715	15.732	7.995	1.00	16.92	A
ATOM	1548	CB	ILE	A	329	25.036	16.451	6.798	1.00	18.22	A
ATOM	1549	CG2	ILE	A	329	25.997	16.493	5.619	1.00	17.39	A
ATOM	1550	CG1	ILE	A	329	23.752	15.733	6.383	1.00	21.82	A
ATOM	1551	CD1	ILE	A	329	23.055	16.386	5.193	1.00	25.55	A
ATOM	1552	C	ILE	A	329	24.784	15.663	9.201	1.00	17.32	A
ATOM	1553	O	ILE	A	329	23.758	14.979	9.179	1.00	18.02	A
ATOM	1554	N	ASN	A	330	25.170	16.349	10.268	1.00	17.70	A
ATOM	1555	CA	ASN	A	330	24.391	16.352	11.497	1.00	18.00	A
ATOM	1556	CB	ASN	A	330	25.208	15.731	12.637	1.00	20.36	A
ATOM	1557	CG	ASN	A	330	25.759	14.353	12.289	1.00	21.76	A
ATOM	1558	OD1	ASN	A	330	25.006	13.418	12.006	1.00	22.43	A
ATOM	1559	ND2	ASN	A	330	27.081	14.223	12.314	1.00	23.90	A

ATOM	1560	C	ASN	A	330	23.979	17.767	11.883	1.00	18.09	A
ATOM	1561	O	ASN	A	330	24.365	18.743	11.235	1.00	16.82	A
ATOM	1562	N	ALA	A	331	23.195	17.868	12.951	1.00	18.79	A
ATOM	1563	CA	ALA	A	331	22.727	19.156	13.441	1.00	19.16	A
ATOM	1564	CB	ALA	A	331	21.802	18.955	14.634	1.00	20.84	A
ATOM	1565	C	ALA	A	331	23.901	20.037	13.837	1.00	18.41	A
ATOM	1566	O	ALA	A	331	23.822	21.261	13.740	1.00	19.60	A
ATOM	1567	N	ASP	A	332	24.989	19.416	14.288	1.00	18.22	A
ATOM	1568	CA	ASP	A	332	26.168	20.170	14.688	1.00	17.37	A
ATOM	1569	CB	ASP	A	332	26.640	19.752	16.090	1.00	19.49	A
ATOM	1570	CG	ASP	A	332	26.835	18.254	16.228	1.00	22.57	A
ATOM	1571	OD1	ASP	A	332	26.695	17.528	15.222	1.00	23.71	A
ATOM	1572	OD2	ASP	A	332	27.136	17.803	17.355	1.00	25.43	A
ATOM	1573	C	ASP	A	332	27.311	20.053	13.689	1.00	16.67	A
ATOM	1574	O	ASP	A	332	28.483	20.038	14.065	1.00	15.11	A
ATOM	1575	N	GLY	A	333	26.959	19.960	12.410	1.00	15.38	A
ATOM	1576	CA	GLY	A	333	27.974	19.897	11.375	1.00	15.75	A
ATOM	1577	C	GLY	A	333	28.344	18.547	10.796	1.00	13.57	A
ATOM	1578	O	GLY	A	333	27.752	17.513	11.111	1.00	14.77	A
ATOM	1579	N	VAL	A	334	29.346	18.580	9.924	1.00	11.52	A
ATOM	1580	CA	VAL	A	334	29.844	17.391	9.254	1.00	10.99	A
ATOM	1581	CB	VAL	A	334	30.746	17.791	8.063	1.00	9.62	A
ATOM	1582	CG1	VAL	A	334	31.534	16.585	7.549	1.00	11.92	A
ATOM	1583	CG2	VAL	A	334	29.879	18.366	6.952	1.00	12.03	A
ATOM	1584	C	VAL	A	334	30.614	16.499	10.218	1.00	11.60	A
ATOM	1585	O	VAL	A	334	31.450	16.965	10.989	1.00	12.63	A
ATOM	1586	N	GLY	A	335	30.301	15.209	10.181	1.00	12.25	A
ATOM	1587	CA	GLY	A	335	30.975	14.252	11.036	1.00	12.89	A
ATOM	1588	C	GLY	A	335	31.193	12.971	10.259	1.00	13.23	A
ATOM	1589	O	GLY	A	335	30.982	12.931	9.048	1.00	13.01	A
ATOM	1590	N	ASP	A	336	31.618	11.916	10.938	1.00	15.14	A
ATOM	1591	CA	ASP	A	336	31.834	10.660	10.244	1.00	16.51	A
ATOM	1592	CB	ASP	A	336	32.956	9.870	10.911	1.00	17.22	A
ATOM	1593	CG	ASP	A	336	34.318	10.457	10.610	1.00	19.47	A
ATOM	1594	OD1	ASP	A	336	34.936	11.045	11.523	1.00	20.13	A
ATOM	1595	OD2	ASP	A	336	34.753	10.345	9.443	1.00	19.26	A
ATOM	1596	C	ASP	A	336	30.561	9.835	10.172	1.00	16.78	A
ATOM	1597	O	ASP	A	336	29.688	9.936	11.034	1.00	16.77	A
ATOM	1598	N	ALA	A	337	30.451	9.039	9.116	1.00	16.17	A
ATOM	1599	CA	ALA	A	337	29.285	8.195	8.920	1.00	17.98	A
ATOM	1600	CB	ALA	A	337	29.267	7.651	7.497	1.00	17.82	A
ATOM	1601	C	ALA	A	337	29.322	7.053	9.926	1.00	19.32	A
ATOM	1602	O	ALA	A	337	30.376	6.472	10.181	1.00	18.99	A
ATOM	1603	N	LYS	A	338	28.163	6.738	10.490	1.00	20.19	A
ATOM	1604	CA	LYS	A	338	28.053	5.676	11.479	1.00	22.21	A
ATOM	1605	CB	LYS	A	338	27.738	6.279	12.850	1.00	23.47	A
ATOM	1606	CG	LYS	A	338	28.784	7.255	13.360	1.00	26.58	A
ATOM	1607	CD	LYS	A	338	30.111	6.561	13.623	1.00	29.32	A
ATOM	1608	CE	LYS	A	338	31.150	7.544	14.142	1.00	32.11	A
ATOM	1609	NZ	LYS	A	338	32.439	6.871	14.460	1.00	34.51	A
ATOM	1610	C	LYS	A	338	26.946	4.702	11.099	1.00	23.93	A
ATOM	1611	O	LYS	A	338	25.977	5.080	10.437	1.00	22.40	A
ATOM	1612	N	ASP	A	339	27.093	3.447	11.508	1.00	25.44	A
ATOM	1613	CA	ASP	A	339	26.068	2.452	11.228	1.00	27.67	A
ATOM	1614	CB	ASP	A	339	26.693	1.085	10.924	1.00	29.98	A
ATOM	1615	CG	ASP	A	339	27.592	.584	12.043	1.00	32.94	A
ATOM	1616	OD1	ASP	A	339	27.427	1.025	13.201	1.00	33.12	A
ATOM	1617	OD2	ASP	A	339	28.462	-.267	11.761	1.00	36.58	A
ATOM	1618	C	ASP	A	339	25.169	2.347	12.456	1.00	28.80	A
ATOM	1619	O	ASP	A	339	24.424	1.352	12.570	1.00	28.88	A
ATOM	1620	OXT	ASP	A	339	25.220	3.279	13.289	1.00	28.59	A
ATOM	1621	CB	PRO		1519	24.486	50.430	-.203	.50	37.27	AC1
ATOM	1622	CG	PRO		1519	24.699	51.944	-.398	.50	37.06	AC1
ATOM	1623	C	PRO		1519	24.307	49.154	1.952	.50	35.98	AC1
ATOM	1624	O	PRO		1519	25.171	48.407	1.497	.50	37.38	AC1
ATOM	1625	N	PRO		1519	24.293	51.611	1.883	.50	34.39	AC1
ATOM	1626	CD	PRO		1519	25.117	52.443	.989	.50	33.96	AC1
ATOM	1627	CA	PRO		1519	23.845	50.392	1.173	.50	35.12	AC1

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ATOM   1628  N   THR B1520      23.744  48.961   3.142  1.00 35.07      B
ATOM   1629  CA  THR B1520      24.098  47.838   4.013  1.00 33.12      B
ATOM   1630  CB  THR B1520      23.242  47.855   5.296  1.00 33.72      B
ATOM   1631  OG1 THR B1520      21.871  47.557   4.982  1.00 33.68      B
ATOM   1632  CG2 THR B1520      23.307  49.243   5.942  1.00 34.95      B
ATOM   1633  C   THR B1520      23.952  46.477   3.357  1.00 31.94      B
ATOM   1634  O   THR B1520      24.698  45.547   3.676  1.00 31.26      B
ATOM   1635  N   LEU B1521      23.026  46.379   2.411  1.00 28.07      B
ATOM   1636  CA  LEU B1521      22.780  45.125   1.720  1.00 27.74      B
ATOM   1637  CB  LEU B1521      21.495  45.232    .896  1.00 27.44      B
ATOM   1638  CG  LEU B1521      20.189  45.382   1.680  1.00 27.21      B
ATOM   1639  CD1 LEU B1521      19.046  45.662    .717  1.00 28.85      B
ATOM   1640  CD2 LEU B1521      19.916  44.121   2.486  1.00 27.53      B
ATOM   1641  C   LEU B1521      23.899  44.613    .817  1.00 26.48      B
ATOM   1642  O   LEU B1521      23.957  43.416    .532  1.00 26.28      B
ATOM   1643  N   LEU B1522      24.783  45.500    .373  1.00 25.12      B
ATOM   1644  CA  LEU B1522      25.854  45.093   -.529  1.00 24.52      B
ATOM   1645  CB  LEU B1522      25.976  46.115  -1.662  1.00 26.00      B
ATOM   1646  CG  LEU B1522      24.681  46.354  -2.447  1.00 27.30      B
ATOM   1647  CD1 LEU B1522      24.911  47.429  -3.496  1.00 28.30      B
ATOM   1648  CD2 LEU B1522      24.221  45.056  -3.097  1.00 26.47      B
ATOM   1649  C   LEU B1522      27.221  44.871    .115  1.00 23.01      B
ATOM   1650  O   LEU B1522      28.192  44.588   -.584  1.00 23.87      B
ATOM   1651  N   GLY B1523      27.303  44.997   1.436  1.00 21.25      B
ATOM   1652  CA  GLY B1523      28.572  44.787   2.114  1.00 19.07      B
ATOM   1653  C   GLY B1523      28.527  43.565   3.013  1.00 16.93      B
ATOM   1654  O   GLY B1523      27.592  42.769   2.933  1.00 18.20      B
ATOM   1655  N   PHE B1524      29.531  43.414   3.872  1.00 15.85      B
ATOM   1656  CA  PHE B1524      29.590  42.278   4.791  1.00 13.68      B
ATOM   1657  CB  PHE B1524      31.027  41.762   4.942  1.00 13.38      B
ATOM   1658  CG  PHE B1524      31.521  40.956   3.776  1.00 12.94      B
ATOM   1659  CD1 PHE B1524      32.085  41.577   2.667  1.00 14.58      B
ATOM   1660  CD2 PHE B1524      31.440  39.568   3.799  1.00 13.15      B
ATOM   1661  CE1 PHE B1524      32.567  40.825   1.594  1.00 12.21      B
ATOM   1662  CE2 PHE B1524      31.914  38.805   2.734  1.00 13.77      B
ATOM   1663  CZ  PHE B1524      32.482  39.437   1.628  1.00 14.06      B
ATOM   1664  C   PHE B1524      29.088  42.622   6.188  1.00 12.65      B
ATOM   1665  O   PHE B1524      29.194  43.762   6.635  1.00 13.98      B
ATOM   1666  N   HIS B1525      28.547  41.613   6.865  1.00 11.84      B
ATOM   1667  CA  HIS B1525      28.078  41.733   8.241  1.00 13.15      B
ATOM   1668  CB  HIS B1525      26.553  41.694   8.327  1.00 15.13      B
ATOM   1669  CG  HIS B1525      25.881  42.936   7.844  1.00 18.82      B
ATOM   1670  CD2 HIS B1525      25.345  43.978   8.521  1.00 20.71      B
ATOM   1671  ND1 HIS B1525      25.675  43.198   6.507  1.00 23.42      B
ATOM   1672  CE1 HIS B1525      25.036  44.349   6.382  1.00 21.27      B
ATOM   1673  NE2 HIS B1525      24.824  44.842   7.589  1.00 22.01      B
ATOM   1674  C   HIS B1525      28.608  40.506   8.977  1.00 12.75      B
ATOM   1675  O   HIS B1525      28.847  39.468   8.358  1.00 12.86      B
ATOM   1676  N   THR B1526      28.812  40.612  10.283  1.00 11.64      B
ATOM   1677  CA  THR B1526      29.261  39.439  11.023  1.00 11.86      B
ATOM   1678  CB  THR B1526      29.661  39.773  12.471  1.00 12.84      B
ATOM   1679  OG1 THR B1526      28.529  40.315  13.165  1.00 14.05      B
ATOM   1680  CG2 THR B1526      30.808  40.768  12.495  1.00 12.72      B
ATOM   1681  C   THR B1526      28.037  38.533  11.065  1.00 12.89      B
ATOM   1682  O   THR B1526      26.927  38.979  10.777  1.00 13.46      B
ATOM   1683  N   ALA B1527      28.222  37.267  11.419  1.00 11.46      B
ATOM   1684  CA  ALA B1527      27.090  36.355  11.486  1.00 14.41      B
ATOM   1685  CB  ALA B1527      27.577  34.923  11.695  1.00 12.82      B
ATOM   1686  C   ALA B1527      26.144  36.771  12.614  1.00 15.41      B
ATOM   1687  O   ALA B1527      25.014  36.286  12.695  1.00 17.98      B
ATOM   1688  N   SER B1528      26.615  37.667  13.480  1.00 16.56      B
ATOM   1689  CA  SER B1528      25.813  38.174  14.593  1.00 19.61      B
ATOM   1690  CB  SER B1528      26.701  38.453  15.816  1.00 19.90      B
ATOM   1691  OG  SER B1528      27.833  39.242  15.479  1.00 23.75      B
ATOM   1692  C   SER B1528      25.045  39.438  14.197  1.00 20.84      B
ATOM   1693  O   SER B1528      24.355  40.041  15.025  1.00 22.21      B
ATOM   1694  N   GLY B1529      25.177  39.840  12.934  1.00 20.05      B
ATOM   1695  CA  GLY B1529      24.463  41.009  12.440  1.00 20.14      B
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ATOM	1696	C	GLY	B1529	25.170	42.352	12.501	1.00	19.33	B
ATOM	1697	O	GLY	B1529	24.563	43.386	12.206	1.00	20.61	B
ATOM	1698	N	LYS	B1530	26.444	42.355	12.873	1.00	17.30	B
ATOM	1699	CA	LYS	B1530	27.201	43.601	12.970	1.00	17.58	B
ATOM	1700	CB	LYS	B1530	28.286	43.475	14.038	1.00	17.52	B
ATOM	1701	CG	LYS	B1530	27.772	43.081	15.411	1.00	21.01	B
ATOM	1702	CD	LYS	B1530	28.925	42.887	16.381	1.00	23.76	B
ATOM	1703	CE	LYS	B1530	28.419	42.487	17.756	1.00	26.60	B
ATOM	1704	NZ	LYS	B1530	27.538	41.296	17.669	1.00	30.15	B
ATOM	1705	C	LYS	B1530	27.853	43.992	11.647	1.00	18.75	B
ATOM	1706	O	LYS	B1530	28.533	43.182	11.018	1.00	17.86	B
ATOM	1707	N	LYS	B1531	27.649	45.237	11.228	1.00	17.05	B
ATOM	1708	CA	LYS	B1531	28.251	45.718	9.991	1.00	19.95	B
ATOM	1709	CB	LYS	B1531	27.836	47.172	9.727	1.00	22.55	B
ATOM	1710	CG	LYS	B1531	28.565	47.851	8.567	1.00	28.55	B
ATOM	1711	CD	LYS	B1531	28.007	47.435	7.215	1.00	34.63	B
ATOM	1712	CE	LYS	B1531	28.704	48.189	6.086	1.00	36.55	B
ATOM	1713	NZ	LYS	B1531	28.094	47.921	4.752	1.00	39.45	B
ATOM	1714	C	LYS	B1531	29.767	45.629	10.134	1.00	19.45	B
ATOM	1715	O	LYS	B1531	30.314	45.892	11.206	1.00	20.19	B
ATOM	1716	N	VAL	B1532	30.446	45.235	9.062	1.00	19.36	B
ATOM	1717	CA	VAL	B1532	31.899	45.140	9.091	1.00	19.78	B
ATOM	1718	CB	VAL	B1532	32.411	43.938	8.268	1.00	19.96	B
ATOM	1719	CG1	VAL	B1532	33.930	43.987	8.162	1.00	19.38	B
ATOM	1720	CG2	VAL	B1532	31.970	42.638	8.919	1.00	19.54	B
ATOM	1721	C	VAL	B1532	32.469	46.419	8.496	1.00	20.72	B
ATOM	1722	O	VAL	B1532	32.213	46.738	7.337	1.00	22.21	B
ATOM	1723	N	LYS	B1533	33.234	47.156	9.295	1.00	22.24	B
ATOM	1724	CA	LYS	B1533	33.826	48.405	8.829	1.00	25.01	B
ATOM	1725	CB	LYS	B1533	34.009	49.375	10.000	1.00	29.14	B
ATOM	1726	CG	LYS	B1533	32.705	49.823	10.635	1.00	33.73	B
ATOM	1727	CD	LYS	B1533	32.941	50.800	11.776	1.00	38.58	B
ATOM	1728	CE	LYS	B1533	33.556	52.098	11.279	1.00	40.70	B
ATOM	1729	NZ	LYS	B1533	33.790	53.054	12.396	1.00	43.43	B
ATOM	1730	C	LYS	B1533	35.166	48.173	8.140	1.00	24.17	B
ATOM	1731	O	LYS	B1533	35.982	47.369	8.592	1.00	24.48	B
ATOM	1732	N	ILE	B1534	35.374	48.882	7.037	1.00	23.24	B
ATOM	1733	CA	ILE	B1534	36.605	48.775	6.264	1.00	24.18	B
ATOM	1734	CB	ILE	B1534	36.326	48.206	4.856	1.00	25.08	B
ATOM	1735	CG2	ILE	B1534	37.633	48.049	4.090	1.00	25.82	B
ATOM	1736	CG1	ILE	B1534	35.604	46.860	4.967	1.00	25.24	B
ATOM	1737	CD1	ILE	B1534	35.219	46.258	3.627	1.00	25.28	B
ATOM	1738	C	ILE	B1534	37.204	50.169	6.111	1.00	23.73	B
ATOM	1739	O	ILE	B1534	36.559	51.064	5.569	1.00	23.27	B
ATOM	1740	N	ALA	B1535	38.430	50.351	6.591	1.00	24.35	B
ATOM	1741	CA	ALA	B1535	39.100	51.645	6.489	1.00	24.68	B
ATOM	1742	CB	ALA	B1535	40.416	51.615	7.254	1.00	24.73	B
ATOM	1743	C	ALA	B1535	39.356	51.984	5.025	1.00	26.08	B
ATOM	1744	O	ALA	B1535	39.755	51.121	4.244	1.00	25.25	B
ATOM	1745	N	LYS	B1536	39.125	53.242	4.655	1.00	26.80	B
ATOM	1746	CA	LYS	B1536	39.335	53.681	3.279	1.00	27.59	B
ATOM	1747	CB	LYS	B1536	39.040	55.178	3.145	1.00	30.55	B
ATOM	1748	CG	LYS	B1536	39.898	56.068	4.032	1.00	34.62	B
ATOM	1749	CD	LYS	B1536	39.565	57.545	3.836	1.00	38.95	B
ATOM	1750	CE	LYS	B1536	39.832	57.994	2.403	1.00	41.45	B
ATOM	1751	NZ	LYS	B1536	39.531	59.441	2.196	1.00	43.50	B
ATOM	1752	C	LYS	B1536	40.762	53.393	2.819	1.00	25.80	B
ATOM	1753	O	LYS	B1536	40.993	53.094	1.646	1.00	26.01	B
ATOM	1754	N	GLU	B1537	41.716	53.485	3.741	1.00	24.83	B
ATOM	1755	CA	GLU	B1537	43.110	53.219	3.409	1.00	24.45	B
ATOM	1756	CB	GLU	B1537	44.029	53.519	4.600	1.00	27.10	B
ATOM	1757	CG	GLU	B1537	44.110	54.984	5.023	1.00	31.85	B
ATOM	1758	CD	GLU	B1537	42.846	55.479	5.698	1.00	35.28	B
ATOM	1759	OE1	GLU	B1537	42.257	54.715	6.492	1.00	35.95	B
ATOM	1760	OE2	GLU	B1537	42.451	56.639	5.449	1.00	37.98	B
ATOM	1761	C	GLU	B1537	43.281	51.756	3.007	1.00	22.80	B
ATOM	1762	O	GLU	B1537	44.055	51.440	2.106	1.00	22.40	B
ATOM	1763	N	SER	B1538	42.556	50.866	3.680	1.00	21.37	B

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ATOM   1764  CA  SER B1538      42.641  49.440   3.382  1.00 20.86      B
ATOM   1765  CB  SER B1538      41.781  48.644   4.366  1.00 21.09      B
ATOM   1766  OG  SER B1538      42.283  48.776   5.684  1.00 23.23      B
ATOM   1767  C   SER B1538      42.211  49.134   1.949  1.00 20.08      B
ATOM   1768  O   SER B1538      42.845  48.333   1.259  1.00 18.25      B
ATOM   1769  N   LEU B1539      41.130  49.769   1.508  1.00 19.51      B
ATOM   1770  CA  LEU B1539      40.635  49.577    .153  1.00 20.82      B
ATOM   1771  CB  LEU B1539      39.276  50.260   -.013  1.00 22.90      B
ATOM   1772  CG  LEU B1539      38.104  49.588    .708  1.00 24.42      B
ATOM   1773  CD1 LEU B1539      36.933  50.553    .816  1.00 26.46      B
ATOM   1774  CD2 LEU B1539      37.705  48.326   -.043  1.00 25.08      B
ATOM   1775  C   LEU B1539      41.638  50.159   -.839  1.00 20.41      B
ATOM   1776  O   LEU B1539      41.880  49.588  -1.903  1.00 20.85      B
ATOM   1777  N   ASP B1540      42.230  51.293   -.481  1.00 20.18      B
ATOM   1778  CA  ASP B1540      43.207  51.936  -1.348  1.00 20.28      B
ATOM   1779  CB  ASP B1540      43.594  53.305   -.776  1.00 23.88      B
ATOM   1780  CG  ASP B1540      44.384  54.147  -1.761  1.00 26.54      B
ATOM   1781  OD1 ASP B1540      43.862  54.414  -2.865  1.00 29.37      B
ATOM   1782  OD2 ASP B1540      45.522  54.547  -1.435  1.00 30.42      B
ATOM   1783  C   ASP B1540      44.453  51.060  -1.490  1.00 20.02      B
ATOM   1784  O   ASP B1540      45.038  50.967  -2.569  1.00 20.33      B
ATOM   1785  N   LYS B1541      44.851  50.413   -.399  1.00 19.20      B
ATOM   1786  CA  LYS B1541      46.035  49.556   -.405  1.00 19.77      B
ATOM   1787  CB  LYS B1541      46.356  49.089   1.019  1.00 21.48      B
ATOM   1788  CG  LYS B1541      46.809  50.212   1.946  1.00 24.88      B
ATOM   1789  CD  LYS B1541      46.941  49.733   3.383  1.00 26.41      B
ATOM   1790  CE  LYS B1541      47.320  50.878   4.309  1.00 28.15      B
ATOM   1791  NZ  LYS B1541      47.277  50.469   5.743  1.00 31.20      B
ATOM   1792  C   LYS B1541      45.918  48.342  -1.328  1.00 19.38      B
ATOM   1793  O   LYS B1541      46.923  47.879  -1.873  1.00 19.13      B
ATOM   1794  N   VAL B1542      44.701  47.836  -1.514  1.00 18.52      B
ATOM   1795  CA  VAL B1542      44.485  46.669  -2.369  1.00 18.69      B
ATOM   1796  CB  VAL B1542      43.539  45.650  -1.685  1.00 18.33      B
ATOM   1797  CG1 VAL B1542      44.121  45.214   -.359  1.00 20.04      B
ATOM   1798  CG2 VAL B1542      42.162  46.264  -1.483  1.00 19.59      B
ATOM   1799  C   VAL B1542      43.906  47.015  -3.740  1.00 18.77      B
ATOM   1800  O   VAL B1542      43.557  46.123  -4.513  1.00 19.16      B
ATOM   1801  N   LYS B1543      43.822  48.309  -4.042  1.00 20.01      B
ATOM   1802  CA  LYS B1543      43.268  48.784  -5.312  1.00 21.69      B
ATOM   1803  CB  LYS B1543      43.488  50.299  -5.444  1.00 23.55      B
ATOM   1804  CG  LYS B1543      44.954  50.700  -5.482  1.00 28.56      B
ATOM   1805  CD  LYS B1543      45.158  52.205  -5.344  1.00 32.47      B
ATOM   1806  CE  LYS B1543      44.767  52.961  -6.600  1.00 35.65      B
ATOM   1807  NZ  LYS B1543      45.188  54.390  -6.512  1.00 38.75      B
ATOM   1808  C   LYS B1543      43.808  48.090  -6.564  1.00 20.66      B
ATOM   1809  O   LYS B1543      43.067  47.879  -7.525  1.00 21.57      B
ATOM   1810  N   ASN B1544      45.088  47.732  -6.556  1.00 20.57      B
ATOM   1811  CA  ASN B1544      45.698  47.090  -7.720  1.00 19.97      B
ATOM   1812  CB  ASN B1544      47.010  47.795  -8.077  1.00 22.42      B
ATOM   1813  CG  ASN B1544      46.817  49.263  -8.392  1.00 24.61      B
ATOM   1814  OD1 ASN B1544      46.018  49.624  -9.257  1.00 26.96      B
ATOM   1815  ND2 ASN B1544      47.553  50.121  -7.692  1.00 26.00      B
ATOM   1816  C   ASN B1544      45.974  45.598  -7.566  1.00 18.50      B
ATOM   1817  O   ASN B1544      46.583  44.989  -8.440  1.00 17.10      B
ATOM   1818  N   LEU B1545      45.518  45.007  -6.469  1.00 17.20      B
ATOM   1819  CA  LEU B1545      45.762  43.591  -6.217  1.00 16.66      B
ATOM   1820  CB  LEU B1545      45.054  43.156  -4.929  1.00 16.31      B
ATOM   1821  CG  LEU B1545      45.166  41.665  -4.598  1.00 16.59      B
ATOM   1822  CD1 LEU B1545      46.622  41.300  -4.352  1.00 16.66      B
ATOM   1823  CD2 LEU B1545      44.319  41.347  -3.379  1.00 17.51      B
ATOM   1824  C   LEU B1545      45.362  42.637  -7.336  1.00 16.69      B
ATOM   1825  O   LEU B1545      46.047  41.641  -7.579  1.00 16.64      B
ATOM   1826  N   PHE B1546      44.258  42.932  -8.014  1.00 16.22      B
ATOM   1827  CA  PHE B1546      43.775  42.047  -9.063  1.00 17.49      B
ATOM   1828  CB  PHE B1546      42.247  41.967  -8.998  1.00 15.66      B
ATOM   1829  CG  PHE B1546      41.737  41.417  -7.699  1.00 11.70      B
ATOM   1830  CD1 PHE B1546      41.945  40.081  -7.366  1.00 13.72      B
ATOM   1831  CD2 PHE B1546      41.099  42.243  -6.780  1.00 13.72      B
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ATOM   1832  CE1 PHE B1546      41.530  39.577  -6.137  1.00 14.70      B
ATOM   1833  CE2 PHE B1546      40.680  41.748  -5.544  1.00 14.99      B
ATOM   1834  CZ  PHE B1546      40.897  40.413  -5.223  1.00 14.37      B
ATOM   1835  C   PHE B1546      44.225  42.384 -10.474  1.00 18.64      B
ATOM   1836  O   PHE B1546      43.774  41.763 -11.432  1.00 19.17      B
ATOM   1837  N   ASP B1547      45.116  43.358 -10.609  1.00 19.30      B
ATOM   1838  CA  ASP B1547      45.602  43.709 -11.934  1.00 22.97      B
ATOM   1839  CB  ASP B1547      46.481  44.962 -11.901  1.00 25.04      B
ATOM   1840  CG  ASP B1547      45.736  46.193 -11.447  1.00 28.33      B
ATOM   1841  OD1 ASP B1547      44.491  46.212 -11.535  1.00 30.07      B
ATOM   1842  OD2 ASP B1547      46.408  47.155 -11.016  1.00 32.49      B
ATOM   1843  C   ASP B1547      46.437  42.557 -12.464  1.00 22.48      B
ATOM   1844  O   ASP B1547      47.139  41.882 -11.712  1.00 24.30      B
ATOM   1845  N   GLU B1548      46.346  42.329 -13.765  1.00 22.96      B
ATOM   1846  CA  GLU B1548      47.118  41.288 -14.413  1.00 22.18      B
ATOM   1847  CB  GLU B1548      46.195  40.276 -15.095  1.00 22.32      B
ATOM   1848  CG  GLU B1548      45.388  39.459 -14.099  1.00 21.84      B
ATOM   1849  CD  GLU B1548      44.480  38.444 -14.759  1.00 21.72      B
ATOM   1850  OE1 GLU B1548      43.684  38.844 -15.632  1.00 20.97      B
ATOM   1851  OE2 GLU B1548      44.558  37.251 -14.396  1.00 23.36      B
ATOM   1852  C   GLU B1548      47.981  42.024 -15.422  1.00 23.17      B
ATOM   1853  O   GLU B1548      47.867  41.829 -16.633  1.00 24.15      B
ATOM   1854  N   LYS B1549      48.825  42.901 -14.886  1.00 22.17      B
ATOM   1855  CA  LYS B1549      49.742  43.713 -15.671  1.00 22.56      B
ATOM   1856  CB  LYS B1549      50.412  44.764 -14.781  1.00 24.49      B
ATOM   1857  CG  LYS B1549      49.486  45.834 -14.236  1.00 29.70      B
ATOM   1858  CD  LYS B1549      49.077  46.801 -15.325  1.00 33.15      B
ATOM   1859  CE  LYS B1549      48.328  47.985 -14.745  1.00 36.67      B
ATOM   1860  NZ  LYS B1549      49.149  48.714 -13.739  1.00 40.31      B
ATOM   1861  C   LYS B1549      50.822  42.838 -16.275  1.00 20.74      B
ATOM   1862  O   LYS B1549      51.222  41.832 -15.687  1.00 20.95      B
ATOM   1863  N   GLU B1550      51.295  43.223 -17.452  1.00 19.67      B
ATOM   1864  CA  GLU B1550      52.353  42.472 -18.099  1.00 20.42      B
ATOM   1865  CB  GLU B1550      52.577  42.987 -19.518  1.00 21.71      B
ATOM   1866  CG  GLU B1550      51.559  42.447 -20.510  1.00 25.16      B
ATOM   1867  CD  GLU B1550      51.666  43.101 -21.867  1.00 27.14      B
ATOM   1868  OE1 GLU B1550      52.801  43.271 -22.360  1.00 28.85      B
ATOM   1869  OE2 GLU B1550      50.611  43.440 -22.443  1.00 30.89      B
ATOM   1870  C   GLU B1550      53.610  42.632 -17.258  1.00 20.42      B
ATOM   1871  O   GLU B1550      53.912  43.722 -16.769  1.00 21.55      B
ATOM   1872  N   GLN B1551      54.329  41.532 -17.082  1.00 19.31      B
ATOM   1873  CA  GLN B1551      55.542  41.516 -16.286  1.00 20.35      B
ATOM   1874  CB  GLN B1551      55.559  40.255 -15.422  1.00 19.40      B
ATOM   1875  CG  GLN B1551      54.349  40.114 -14.521  1.00 19.34      B
ATOM   1876  CD  GLN B1551      54.267  41.231 -13.504  1.00 22.39      B
ATOM   1877  OE1 GLN B1551      55.221  41.481 -12.770  1.00 21.26      B
ATOM   1878  NE2 GLN B1551      53.127  41.908 -13.455  1.00 22.77      B
ATOM   1879  C   GLN B1551      56.782  41.541 -17.170  1.00 21.10      B
ATOM   1880  O   GLN B1551      56.683  41.486 -18.395  1.00 21.97      B
ATOM   1881  N   THR B1552      57.949  41.639 -16.544  1.00 22.64      B
ATOM   1882  CA  THR B1552      59.201  41.634 -17.288  1.00 25.11      B
ATOM   1883  CB  THR B1552      60.332  42.316 -16.497  1.00 27.42      B
ATOM   1884  OG1 THR B1552      59.999  43.692 -16.281  1.00 29.24      B
ATOM   1885  CG2 THR B1552      61.645  42.228 -17.265  1.00 27.94      B
ATOM   1886  C   THR B1552      59.567  40.172 -17.505  1.00 25.06      B
ATOM   1887  O   THR B1552      59.769  39.432 -16.545  1.00 25.65      B
ATOM   1888  N   GLY B1553      59.637  39.756 -18.764  1.00 25.65      B
ATOM   1889  CA  GLY B1553      59.967  38.373 -19.057  1.00 25.06      B
ATOM   1890  C   GLY B1553      61.378  38.190 -19.573  1.00 26.56      B
ATOM   1891  O   GLY B1553      61.927  39.065 -20.242  1.00 26.49      B
ATOM   1892  N   SER B1554      61.972  37.046 -19.255  1.00 28.84      B
ATOM   1893  CA  SER B1554      63.325  36.743 -19.702  1.00 30.62      B
ATOM   1894  CB  SER B1554      64.346  37.283 -18.696  1.00 32.10      B
ATOM   1895  OG  SER B1554      64.127  36.745 -17.401  1.00 33.78      B
ATOM   1896  C   SER B1554      63.510  35.238 -19.872  1.00 30.37      B
ATOM   1897  O   SER B1554      62.646  34.475 -19.388  1.00 31.99      B
ATOM   1898  OXT SER B1554      64.523  34.841 -20.486  1.00 33.32      B
ATOM   1899  C   GLY C   1      23.040  64.501  10.728  1.00 25.62      C
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ATOM   1900  O   GLY C   1      22.550  63.402  10.981  1.00 24.58      C
ATOM   1901  N   GLY C   1      23.653  64.653  13.149  1.00 26.62      C
ATOM   1902  CA  GLY C   1      23.720  65.313  11.814  1.00 25.97      C
ATOM   1903  N   SER C   2      23.029  65.034   9.509  1.00 24.78      C
ATOM   1904  CA  SER C   2      22.384  64.364   8.385  1.00 25.77      C
ATOM   1905  CB  SER C   2      21.632  65.390   7.535  1.00 24.41      C
ATOM   1906  OG  SER C   2      20.677  66.091   8.309  1.00 23.97      C
ATOM   1907  C   SER C   2      23.325  63.569   7.486  1.00 26.68      C
ATOM   1908  O   SER C   2      22.896  63.028   6.467  1.00 25.80      C
ATOM   1909  N   MSE C   3      24.601  63.496   7.847  1.00 28.16      C
ATOM   1910  CA  MSE C   3      25.553  62.751   7.031  1.00 31.64      C
ATOM   1911  CB  MSE C   3      26.938  62.778   7.670  1.00 33.78      C
ATOM   1912  CG  MSE C   3      28.000  62.090   6.840  1.00 38.54      C
ATOM   1913  SE  MSE C   3      29.693  62.045   7.747  1.00 49.47      C
ATOM   1914  CE  MSE C   3      30.391  63.745   7.182  1.00 43.04      C
ATOM   1915  C   MSE C   3      25.087  61.305   6.881  1.00 32.89      C
ATOM   1916  O   MSE C   3      24.652  60.685   7.851  1.00 32.94      C
ATOM   1917  N   GLY C   4      25.182  60.771   5.665  1.00 34.65      C
ATOM   1918  CA  GLY C   4      24.754  59.401   5.437  1.00 36.89      C
ATOM   1919  C   GLY C   4      25.681  58.384   6.070  1.00 38.07      C
ATOM   1920  O   GLY C   4      26.885  58.684   6.213  1.00 38.86      C
ATOM   1921  OXT GLY C   4      25.207  57.277   6.411  1.00 40.87      C
ATOM   1922  O   HOH     1      27.203  32.665  -8.545  1.00 12.07
ATOM   1923  O   HOH     2      31.152  37.373 -10.128  1.00 14.68
ATOM   1924  O   HOH     3      24.813  29.097   1.505  1.00 19.02
ATOM   1925  O   HOH     4      41.055  25.105   -.319  1.00 11.16
ATOM   1926  O   HOH     5      43.681  37.645   6.233  1.00 14.81
ATOM   1927  O   HOH     6      45.327  22.607  11.105  1.00 13.75
ATOM   1928  O   HOH     7      39.600  31.034 -14.585  1.00 13.20
ATOM   1929  O   HOH     8      43.640  26.446  -6.581  1.00 14.05
ATOM   1930  O   HOH     9      25.339  14.708  -6.366  1.00 21.76
ATOM   1931  O   HOH    10      47.852  25.013  18.123  1.00 15.00
ATOM   1932  O   HOH    11      41.038  31.746 -16.720  1.00 15.00
ATOM   1933  O   HOH    12      34.703  38.853 -12.674  1.00 14.66
ATOM   1934  O   HOH    13      41.935  21.373   -.230  1.00 15.53
ATOM   1935  O   HOH    14      33.052   8.732   7.686  1.00 17.18
ATOM   1936  O   HOH    15      29.065  32.805  23.625  1.00 22.84
ATOM   1937  O   HOH    16      39.100  42.813   8.664  1.00 24.97
ATOM   1938  O   HOH    17      45.225  34.430 -10.500  1.00 14.90
ATOM   1939  O   HOH    18      34.758   6.368   4.080  1.00 20.01
ATOM   1940  O   HOH    19      27.240  27.751  20.443  1.00 18.69
ATOM   1941  O   HOH    20      50.907  39.282 -16.750  1.00 20.51
ATOM   1942  O   HOH    21      47.270  47.282  -4.465  1.00 21.63
ATOM   1943  O   HOH    22      40.136  25.218  21.558  1.00 19.04
ATOM   1944  O   HOH    23      26.144   8.662  10.277  1.00 18.32
ATOM   1945  O   HOH    24      42.725  45.381  -8.655  1.00 27.15
ATOM   1946  O   HOH    25      40.507  26.175 -10.534  1.00 24.50
ATOM   1947  O   HOH    26      28.530  16.165  13.719  1.00 33.54
ATOM   1948  O   HOH    27      49.779  14.277   1.640  1.00 26.13
ATOM   1949  O   HOH    28      37.754  17.604  13.513  1.00 21.28
ATOM   1950  O   HOH    29      25.719  40.907   4.909  1.00 26.13
ATOM   1951  O   HOH    30      46.444  34.888 -14.485  1.00 30.70
ATOM   1952  O   HOH    31      42.905  22.704  -2.761  1.00 21.06
ATOM   1953  O   HOH    32      45.201  36.882 -11.552  1.00 28.24
ATOM   1954  O   HOH    33      25.649  19.886   8.886  1.00 28.23
ATOM   1955  O   HOH    34      26.045  10.696  12.207  1.00 26.17
ATOM   1956  O   HOH    35      32.469  36.471  23.268  1.00 30.94
ATOM   1957  O   HOH    36      45.943  28.640  19.548  1.00 23.84
ATOM   1958  O   HOH    37      43.494  30.640 -16.264  1.00 19.57
ATOM   1959  O   HOH    38      40.052  27.988  21.059  1.00 19.96
ATOM   1960  O   HOH    39      30.163  11.427  -5.817  1.00 23.16
ATOM   1961  O   HOH    40      22.655  26.060  -1.019  1.00 25.88
ATOM   1962  O   HOH    41      47.443  25.123  -1.056  1.00 26.06
ATOM   1963  O   HOH    42      43.351  38.717 -10.710  1.00 31.36
ATOM   1964  O   HOH    43      47.439  22.148   9.534  1.00 23.85
ATOM   1965  O   HOH    44      39.265   8.211   3.837  1.00 24.72
ATOM   1966  O   HOH    45      29.442  47.107  13.465  1.00 28.59
ATOM   1967  O   HOH    46      49.276  48.894  -1.723  1.00 23.41
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ATOM	1968	O	HOH	47	36.013	33.810	24.513	1.00	26.17
ATOM	1969	O	HOH	48	41.724	36.316	13.254	1.00	25.30
ATOM	1970	O	HOH	49	38.645	15.363	-8.356	1.00	24.55
ATOM	1971	O	HOH	50	31.955	12.217	13.710	1.00	26.51
ATOM	1972	O	HOH	51	45.068	55.619	1.338	1.00	27.50
ATOM	1973	O	HOH	52	43.052	19.153	9.777	1.00	23.61
ATOM	1974	O	HOH	53	45.777	32.997	-12.641	1.00	28.74
ATOM	1975	O	HOH	54	28.793	15.549	-7.585	1.00	26.71
ATOM	1976	O	HOH	55	49.821	42.639	-12.216	1.00	30.32
ATOM	1977	O	HOH	56	21.473	35.733	-4.098	1.00	21.73
ATOM	1978	O	HOH	57	42.925	18.920	-.016	1.00	30.56
ATOM	1979	O	HOH	58	28.680	-.098	15.206	1.00	24.41
ATOM	1980	O	HOH	59	30.575	22.738	24.395	1.00	28.00
ATOM	1981	O	HOH	60	17.766	10.990	3.488	1.00	31.85
ATOM	1982	O	HOH	61	49.649	49.378	-5.610	1.00	38.05
ATOM	1983	O	HOH	62	47.518	52.219	-2.812	1.00	26.66
ATOM	1984	O	HOH	63	41.787	11.851	9.383	1.00	31.75
ATOM	1985	O	HOH	64	19.342	13.836	4.361	1.00	26.81
ATOM	1986	O	HOH	65	28.428	11.606	12.742	1.00	32.86
ATOM	1987	O	HOH	66	26.186	41.935	.560	1.00	29.32
ATOM	1988	O	HOH	67	29.916	3.091	12.731	1.00	35.96
ATOM	1989	O	HOH	68	32.525	39.422	-19.919	1.00	28.79
ATOM	1990	O	HOH	69	23.391	12.991	-5.165	1.00	27.70
ATOM	1991	O	HOH	70	37.988	45.231	8.061	1.00	31.23
ATOM	1992	O	HOH	71	51.112	27.635	-9.569	1.00	27.13
ATOM	1993	O	HOH	72	44.253	30.674	-13.637	1.00	26.48
ATOM	1994	O	HOH	73	50.881	30.964	-3.729	1.00	34.82
ATOM	1995	O	HOH	74	40.933	28.825	-10.989	1.00	42.43
ATOM	1996	O	HOH	75	27.184	22.223	9.119	1.00	27.88
ATOM	1997	O	HOH	76	34.540	39.110	11.358	1.00	40.78
ATOM	1998	O	HOH	77	46.502	22.169	-3.457	1.00	30.26
ATOM	1999	O	HOH	78	53.219	46.329	-17.171	1.00	28.75
ATOM	2000	O	HOH	79	26.474	24.441	-5.560	1.00	27.23
ATOM	2001	O	HOH	80	21.166	23.641	-4.948	1.00	35.36
ATOM	2002	O	HOH	81	46.816	32.597	16.414	1.00	35.59
ATOM	2003	O	HOH	82	29.879	14.101	14.638	1.00	31.68
ATOM	2004	O	HOH	83	21.692	33.500	2.984	1.00	30.16
ATOM	2005	O	HOH	84	29.295	27.121	22.187	1.00	25.57
ATOM	2006	O	HOH	85	28.731	12.779	-8.089	1.00	38.33
ATOM	2007	O	HOH	86	27.280	16.834	-9.400	1.00	46.09
ATOM	2008	O	HOH	87	26.071	25.682	-7.687	1.00	35.23
ATOM	2009	O	HOH	88	31.705	45.557	4.386	1.00	36.53
ATOM	2010	O	HOH	89	42.737	27.677	-16.494	1.00	43.50
ATOM	2011	O	HOH	90	35.195	13.995	13.837	1.00	34.72
ATOM	2012	O	HOH	91	49.946	45.582	-18.866	1.00	29.05
ATOM	2013	O	HOH	92	49.674	15.137	4.173	1.00	42.43
ATOM	2014	O	HOH	93	24.992	40.863	2.394	1.00	29.44
ATOM	2015	O	HOH	94	35.938	29.931	22.590	1.00	33.47
ATOM	2016	O	HOH	95	36.358	31.790	18.073	1.00	38.64
ATOM	2017	O	HOH	96	47.419	54.724	-3.794	1.00	29.22
ATOM	2018	O	HOH	97	47.298	25.185	-13.959	1.00	27.59
ATOM	2019	O	HOH	98	49.410	31.445	-.598	1.00	37.89
ATOM	2020	O	HOH	99	32.034	44.105	-10.298	1.00	32.29
ATOM	2021	O	HOH	100	46.589	20.057	12.718	1.00	35.82
ATOM	2022	O	HOH	101	40.404	18.582	19.335	1.00	37.38
ATOM	2023	O	HOH	102	36.397	37.290	23.171	1.00	38.30
ATOM	2024	O	HOH	103	45.419	35.806	6.232	1.00	39.97
ATOM	2025	O	HOH	104	39.400	18.431	15.599	1.00	28.80
ATOM	2026	O	HOH	105	32.747	22.249	25.771	1.00	35.21
ATOM	2027	O	HOH	106	31.993	43.225	-12.811	1.00	31.67
ATOM	2028	O	HOH	107	36.965	41.556	8.934	1.00	34.98
ATOM	2029	O	HOH	108	28.311	37.534	18.638	1.00	41.87
ATOM	2030	O	HOH	109	43.152	40.996	-17.014	1.00	34.31
ATOM	2031	O	HOH	110	36.900	23.769	24.433	1.00	36.25
ATOM	2032	O	HOH	111	22.163	15.646	14.398	1.00	36.85
ATOM	2033	O	HOH	112	35.492	21.090	24.155	1.00	42.67
ATOM	2034	O	HOH	113	48.632	28.953	2.985	1.00	31.18
ATOM	2035	O	HOH	114	39.959	28.401	-13.559	1.00	38.45

ATOM	2036	O	HOH	115	32.211	44.343	12.977	1.00	35.11
ATOM	2037	O	HOH	116	57.018	43.358	-20.359	1.00	34.09
ATOM	2038	O	HOH	117	43.928	36.491	15.046	1.00	44.76
ATOM	2039	O	HOH	118	41.009	17.495	-8.021	1.00	28.89
ATOM	2040	O	HOH	119	47.866	53.440	6.326	1.00	43.86
ATOM	2041	O	HOH	120	19.063	32.664	8.432	1.00	51.10
ATOM	2042	O	HOH	121	35.431	41.465	11.175	1.00	35.75
ATOM	2043	O	HOH	122	41.401	44.934	-4.130	1.00	32.52
ATOM	2044	O	HOH	123	43.399	15.096	-1.902	1.00	35.28
ATOM	2045	O	HOH	124	50.234	39.780	-12.613	1.00	40.18
ATOM	2046	O	HOH	125	43.037	30.072	18.750	1.00	45.64
ATOM	2047	O	HOH	126	44.652	33.989	15.169	1.00	36.16
ATOM	2048	O	HOH	127	38.229	48.920	9.835	1.00	47.09
ATOM	2049	O	HOH	128	44.947	18.550	19.997	1.00	36.95
ATOM	2050	O	HOH	129	19.249	33.307	-4.291	1.00	35.52
ATOM	2051	O	HOH	130	20.932	42.677	5.492	1.00	38.75
ATOM	2052	O	HOH	131	32.240	5.674	-7.678	1.00	42.41
ATOM	2053	O	HOH	132	25.079	5.184	2.319	1.00	43.83
ATOM	2054	O	HOH	133	47.452	34.447	-8.833	1.00	33.02
ATOM	2055	O	HOH	134	31.823	25.421	-14.083	1.00	43.26
ATOM	2056	O	HOH	135	21.662	1.721	13.249	1.00	37.77
ATOM	2057	O	HOH	136	43.284	20.715	-10.461	1.00	32.13
ATOM	2058	O	HOH	137	23.845	9.069	-4.875	1.00	37.96
ATOM	2059	O	HOH	138	42.205	23.336	-17.516	1.00	39.25
ATOM	2060	O	HOH	139	23.782	47.257	8.875	1.00	36.18
ATOM	2061	O	HOH	140	40.071	29.109	18.652	1.00	36.37
ATOM	2062	O	HOH	141	50.037	23.125	9.649	1.00	45.98
ATOM	2063	O	HOH	142	19.583	34.873	10.411	1.00	47.78
ATOM	2064	O	HOH	143	43.464	17.607	18.095	1.00	47.57
ATOM	2065	O	HOH	144	25.361	15.356	16.333	1.00	41.25
ATOM	2066	O	HOH	145	28.757	38.927	-17.342	1.00	34.49
ATOM	2067	O	HOH	146	23.938	-1.305	12.858	1.00	51.98
ATOM	2068	O	HOH	147	33.517	18.774	-13.399	1.00	46.54
ATOM	2069	O	HOH	148	49.091	33.188	18.209	1.00	46.77
ATOM	2070	O	HOH	149	50.357	27.234	-.902	1.00	40.05
ATOM	2071	O	HOH	150	25.608	6.521	-2.912	1.00	43.02
ATOM	2072	O	HOH	151	38.264	4.869	-2.160	1.00	38.27
ATOM	2073	O	HOH	152	62.716	38.725	-15.633	1.00	47.64
ATOM	2074	O	HOH	153	47.852	13.446	6.230	1.00	45.10
ATOM	2075	O	HOH	154	30.371	42.873	-21.841	1.00	49.83
ATOM	2076	O	HOH	155	25.807	26.178	-10.206	1.00	41.92
ATOM	2077	O	HOH	156	20.377	17.443	-2.962	1.00	37.23
ATOM	2078	O	HOH	157	26.310	19.158	-9.197	1.00	40.75
ATOM	2079	O	HOH	158	44.764	43.862	-15.074	1.00	46.84
ATOM	2080	O	HOH	159	38.089	28.511	23.290	1.00	52.16
ATOM	2081	O	HOH	160	39.671	34.256	14.970	1.00	52.34
ATOM	2082	O	HOH	161	20.912	34.446	6.722	1.00	51.80
ATOM	2083	O	HOH	162	47.355	17.692	16.464	1.00	44.35
ATOM	2084	O	HOH	163	40.877	24.164	-19.590	1.00	50.62
ATOM	2085	O	HOH	164	22.739	41.807	2.902	1.00	45.77
ATOM	2086	O	HOH	165	19.295	40.596	-6.896	1.00	40.71
ATOM	2087	O	HOH	166	44.688	45.877	11.462	1.00	49.75
ATOM	2088	O	HOH	167	65.941	38.623	-21.101	1.00	41.18
ATOM	2089	O	HOH	168	20.892	37.818	3.324	1.00	36.26
ATOM	2090	O	HOH	169	23.791	54.770	-.960	1.00	47.88
ATOM	2091	O	HOH	170	37.603	28.849	-15.685	1.00	40.98
ATOM	2092	O	HOH	171	45.555	18.839	.687	1.00	36.06
ATOM	2093	O	HOH	172	35.456	41.167	-13.948	1.00	25.05
ATOM	2094	O	HOH	173	31.200	38.910	-25.308	1.00	37.28
ATOM	2095	O	HOH	174	21.554	13.921	10.766	1.00	36.99
ATOM	2096	O	HOH	175	46.026	26.992	-15.385	1.00	39.58
ATOM	2097	O	HOH	176	37.903	17.801	18.592	1.00	48.95
ATOM	2098	O	HOH	177	43.747	13.395	8.035	1.00	39.48
ATOM	2099	O	HOH	178	34.071	38.400	19.794	1.00	35.56
ATOM	2100	O	HOH	179	43.250	39.476	13.165	1.00	37.82
ATOM	2101	O	HOH	180	41.483	7.783	2.019	1.00	45.02
ATOM	2102	O	HOH	181	65.389	34.398	-23.115	1.00	42.44
ATOM	2103	O	HOH	182	33.931	41.093	14.772	1.00	41.75

ATOM	2104	O	HOH	183	20.394	26.531	-2.994	1.00	45.01
ATOM	2105	O	HOH	184	46.284	41.009	9.919	1.00	41.10
ATOM	2106	O	HOH	185	47.034	40.049	-9.804	1.00	36.98
ATOM	2107	O	HOH	186	49.956	29.227	.659	1.00	41.68
ATOM	2108	O	HOH	187	25.126	33.755	20.531	1.00	45.06
ATOM	2109	O	HOH	188	45.660	12.088	6.545	1.00	47.03
ATOM	2110	O	HOH	189	53.064	31.023	-2.009	1.00	44.55
ATOM	2111	O	HOH	190	21.902	54.378	-2.782	1.00	45.52
ATOM	2112	O	HOH	191	47.488	40.412	5.641	1.00	38.47
ATOM	2113	O	HOH	192	23.372	38.108	-12.261	1.00	36.78
ATOM	2114	O	HOH	193	32.823	6.238	8.957	1.00	31.69
ATOM	2115	O	HOH	194	21.776	33.149	15.893	1.00	43.71
ATOM	2116	O	HOH	195	25.948	2.717	3.211	1.00	41.21
ATOM	2117	O	HOH	196	37.457	24.842	-16.507	1.00	48.71
ATOM	2118	O	HOH	197	25.655	4.669	-.498	1.00	41.01
ATOM	2119	O	HOH	198	34.993	41.490	-16.488	1.00	42.97
ATOM	2120	O	HOH	199	51.572	32.788	-1.315	1.00	41.87
ATOM	2121	O	HOH	200	34.147	30.225	-17.326	1.00	37.43
ATOM	2122	O	HOH	201	55.135	44.572	-21.602	1.00	41.06
ATOM	2123	O	HOH	202	25.757	45.671	-7.830	1.00	44.53
ATOM	2124	O	HOH	203	37.549	6.250	2.375	1.00	38.07
ATOM	2125	O	HOH	204	16.646	31.917	2.952	1.00	42.39
ATOM	2126	O	HOH	205	49.733	40.229	1.785	1.00	43.85
ATOM	2127	O	HOH	206	46.253	39.703	7.766	1.00	42.68
ATOM	2128	O	HOH	207	37.677	35.948	18.903	1.00	45.70
ATOM	2129	O	HOH	208	23.633	36.693	17.352	1.00	40.00
ATOM	2130	O	HOH	209	54.776	29.648	2.106	1.00	45.43
ATOM	2131	O	HOH	210	27.204	25.113	-13.388	1.00	42.37
ATOM	2132	O	HOH	211	16.997	29.300	-.454	1.00	42.78
ATOM	2133	O	HOH	212	44.578	21.178	-4.267	1.00	45.11
ATOM	2134	O	HOH	213	34.450	39.857	-18.339	1.00	40.15
ATOM	2135	O	HOH	214	48.993	29.855	-2.640	1.00	48.30
ATOM	2136	O	HOH	215	47.166	30.914	6.435	1.00	40.03
ATOM	2137	O	HOH	216	24.477	38.679	9.302	1.00	44.85
ATOM	2138	O	HOH	217	40.570	31.936	15.567	1.00	39.55
ATOM	2139	O	HOH	218	47.679	19.437	9.176	1.00	46.30
ATOM	2140	O	HOH	219	49.467	32.411	20.725	1.00	49.57
ATOM	2141	O	HOH	220	40.564	48.980	-8.727	1.00	38.53
ATOM	2142	O	HOH	221	51.817	27.969	14.989	1.00	45.36
ATOM	2143	O	HOH	222	45.303	19.657	10.595	1.00	50.38
ATOM	2144	O	HOH	223	37.514	51.784	9.970	1.00	45.01
ATOM	2145	O	HOH	224	23.691	17.281	-6.725	1.00	34.27
ATOM	2146	O	HOH	225	39.832	6.213	-.004	1.00	43.18
ATOM	2147	O	HOH	226	14.435	31.992	6.539	1.00	40.54
ATOM	2148	O	HOH	227	28.440	3.081	-.375	1.00	40.66
ATOM	2149	O	HOH	228	32.185	1.604	-.032	1.00	39.88
ATOM	2150	O	HOH	229	31.504	47.620	2.802	1.00	38.71
ATOM	2151	O	HOH	230	43.339	48.665	-10.895	1.00	40.50
ATOM	2152	O	HOH	231	48.992	42.900	-8.868	1.00	40.18
ATOM	2153	O	HOH	232	50.311	46.431	-10.063	1.00	38.69
ATOM	2154	O	HOH	233	45.885	49.961	-12.873	1.00	42.42
ATOM	2155	O	HOH	234	21.172	36.234	8.566	1.00	42.66
ATOM	2156	O	HOH	235	19.309	10.393	10.198	1.00	38.58
ATOM	2157	O	HOH	236	35.310	7.159	11.114	1.00	38.88
ATOM	2158	O	HOH	237	48.544	43.963	6.735	1.00	41.80
ATOM	2159	O	HOH	238	37.971	55.166	6.733	1.00	39.07
ATOM	2160	O	HOH	239	32.689	38.646	24.608	1.00	39.11
ATOM	2161	O	HOH	240	36.473	38.193	18.321	1.00	41.71
ATOM	2162	O	HOH	241	25.507	41.267	-12.919	1.00	35.13
ATOM	2163	O	HOH	242	23.143	35.618	-15.172	1.00	39.82
ATOM	2164	O	HOH	243	49.140	33.897	5.783	1.00	40.42
ATOM	2165	O	HOH	244	29.532	27.579	-16.268	1.00	39.77
ATOM	2166	O	HOH	245	26.507	50.321	5.926	1.00	35.74
ATOM	2167	O	HOH	246	24.886	49.944	8.651	1.00	37.76
ATOM	2168	O	HOH	247	33.171	50.567	6.460	1.00	35.10
ATOM	2169	C1	EDO	1	49.678	27.876	17.913	1.00	32.33
ATOM	2170	O1	EDO	1	48.324	27.636	18.334	1.00	32.24
ATOM	2171	C2	EDO	1	49.859	29.331	17.617	1.00	33.08

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ATOM   2172  O2  EDO     1      49.776  29.707  16.203  1.00 33.95
ATOM   2173  C1  EDO     2      35.821  26.057 -12.559  1.00 27.36
ATOM   2174  O1  EDO     2      35.083  24.825 -12.633  1.00 26.99
ATOM   2175  C2  EDO     2      37.288  25.766 -12.507  1.00 27.04
ATOM   2176  O2  EDO     2      37.823  25.421 -11.188  1.00 26.81
ATOM   2177  C1  EDO     3      32.109   4.707  -1.196  1.00 32.05
ATOM   2178  O1  EDO     3      30.999   3.924   -.720  1.00 34.90
ATOM   2179  C2  EDO     3      32.483   5.724   -.166  1.00 30.33
ATOM   2180  O2  EDO     3      33.342   5.246    .915  1.00 32.01
ATOM   2181  C1  EDO     4      20.413  30.402  -8.539  1.00 38.13
ATOM   2182  O1  EDO     4      20.666  29.723  -7.292  1.00 38.27
ATOM   2183  C2  EDO     4      20.600  31.879  -8.368  1.00 38.37
ATOM   2184  O2  EDO     4      20.800  32.350  -6.995  1.00 38.66
ATOM   2185  C1  EDO     5      21.662  24.418   7.348  1.00 35.45
ATOM   2186  O1  EDO     5      23.030  24.437   7.797  1.00 36.25
ATOM   2187  C2  EDO     5      21.624  24.463   5.852  1.00 35.50
ATOM   2188  O2  EDO     5      21.767  25.789   5.249  1.00 36.44
ATOM   2189 MG+2 MG2     1      43.852  18.841   2.109  1.00 27.78
ATOM   2190 CL-1 CL1     1      24.304  20.875   1.803  1.00 17.97
ATOM   2191  N   MSE   158      35.110  34.014   5.907   .44 10.21       AC2
ATOM   2192  CA  MSE   158      34.354  34.920   5.054   .44 11.98       AC2
ATOM   2193  CB  MSE   158      35.299  35.639   4.091   .44 15.25       AC2
ATOM   2194  CG  MSE   158      34.663  36.759   3.292   .44 19.01       AC2
ATOM   2195  SE  MSE   158      35.246  38.493   3.909   .44 26.38       AC2
ATOM   2196  CE  MSE   158      37.144  38.257   3.682   .44 20.56       AC2
ATOM   2197  C   MSE   158      33.395  34.019   4.277   .44 11.27       AC2
ATOM   2198  O   MSE   158      33.821  33.037   3.669   .44 11.23       AC2
ATOM   2199  N   SER   208      39.368  41.606    .024   .50  5.19       AC2
ATOM   2200  CA  SER   208      40.803  41.859    .059   .50  6.96       AC2
ATOM   2201  CB  SER   208      41.287  42.307  -1.316   .50  6.77       AC2
ATOM   2202  OG  SER   208      41.093  41.278  -2.266   .50 12.86       AC2
ATOM   2203  C   SER   208      41.172  42.904   1.102   .50  5.34       AC2
ATOM   2204  O   SER   208      42.168  42.759   1.808   .50  2.94       AC2
ATOM   2205  N   ILE   220      34.627  31.400   1.641   .50  1.35       AC2
ATOM   2206  CA  ILE   220      33.627  30.506   1.061   .50  1.35       AC2
ATOM   2207  CB  ILE   220      32.618  30.008   2.134   .50  1.35       AC2
ATOM   2208  CG2 ILE   220      31.422  29.326   1.458   .50  1.35       AC2
ATOM   2209  CG1 ILE   220      33.312  29.085   3.141   .50  1.97       AC2
ATOM   2210  CD1 ILE   220      33.863  27.818   2.556   .50  8.09       AC2
ATOM   2211  C   ILE   220      32.807  31.257    .020   .50  1.35       AC2
ATOM   2212  O   ILE   220      32.421  32.406    .246   .50  1.35       AC2
ATOM   2213  N   MSE   326      33.175   8.443   2.911   .39 17.50       AC2
ATOM   2214  CA  MSE   326      31.818   8.709   3.360   .39 17.68       AC2
ATOM   2215  CB  MSE   326      31.105   7.414   3.748   .39 21.36       AC2
ATOM   2216  CG  MSE   326      30.708   6.543   2.581   .39 24.62       AC2
ATOM   2217  SE  MSE   326      29.821   4.948   3.175   .39 34.10       AC2
ATOM   2218  CE  MSE   326      27.998   5.567   3.081   .39 30.04       AC2
ATOM   2219  C   MSE   326      31.873   9.621   4.568   .39 16.52       AC2
ATOM   2220  O   MSE   326      32.839   9.602   5.331   .39 17.10       AC2
ATOM   2221  CB  PRO  1519      23.711  50.412    .520   .50 37.35       AC2
ATOM   2222  CG  PRO  1519      24.961  50.755   -.261   .50 38.95       AC2
ATOM   2223  C   PRO  1519      24.595  49.927   2.807   .50 36.73       AC2
ATOM   2224  O   PRO  1519      25.750  49.985   3.197   .50 37.75       AC2
ATOM   2225  N   PRO  1519      25.010  52.092   1.661   .50 38.05       AC2
ATOM   2226  CD  PRO  1519      25.361  52.159    .229   .50 38.46       AC2
ATOM   2227  CA  PRO  1519      24.029  50.997   1.887   .50 37.02       AC2
END
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FIGURE 2

Table 2 **Crystallographic data on the BRC4-RAD51 complex.**

Diffraction data (space group: $P2_12_12_1$: *a*=57.30Å, *b*=59.14Å, *c*=77.20Å)

Dataset	Resolution	Wavelength	Reflections[1] (unique)	Completeness (outer shell)	R_{sym}[2] (outer shell)	I/σ(I)	Beamline
Native	1.8Å	1.5418Å	169388 (24702)	99.9 (99.1)	0.051 (0.308)	40.9 (6.7)	In-house
$KAu(CN)_2$	2.0Å	1.5418Å	179758 (18077)	100.0 (100.0)	0.059 (0.194)	36.6 (11.9)	In-house
SeMet, peak	1.7Å	0.9792Å	204230 (29143)	99.9 (99.9)	0.077 (0.321)	23.5 (6.5)	ESRF, ID-29
SeMet, remote	1.7Å	0.90831Å	207259 (29329)	99.9 (99.6)	0.070 (0.481)	24.7 (4.2)	ESRF, ID-29

Phasing

	$KAu(CN)_2$	SeMet, peak	SeMet, remote
Rcullis (iso/ano)[3]	0.93 / 0.95	-, 0.70	0.84 / 0.84
Phasing power (iso/ano)[4]	0.72 / 0.74	-, 2.1	0.48 / 1.65
Figure of merit[5]	0.21	0.51	

Refinement[6]

Resolution (Å)	Reflections	Number of non-H atoms	R[7] (%)	R_{free} (%)	<B> (A^2)	Rmsd bonds (Å)	Rmsd angles (°)
24.8-1.7	55746	2179	19.1	20.6	21.1	0.006	1.229

[1] For MAD data, the Bijvoet pairs were not merged.

[2] $R_{sym} = \sum_{hkl}\sum_{i}\left|I_i(hkl) - \langle I_i(hkl)\rangle\right| \Big/ \sum_{hkl}\sum_{i} I_i(hkl)$

[3] R_{cullis} as defined in SHARP.

[4] Phasing power as defined in SHARP.

[5] Figure of merit as defined in SHARP.

[6] Statistics for all data.

[7] R-factor = $\sum_{hkl}\left|\,|F_{obs}| - |F_{calc}|\,\right| \Big/ \sum_{hkl}|F_{obs}|$

FIGURE 3

Table 3 **Structure-based analysis of BRCA2 BRC sequence conservation.**

				β	β	β				β	β	β				α	α	α	α	α	α	α						
	L	L	G	F	H	T	A	S	G	K	K	V	K	I	A	K	E	S	L	D	K	V	K	N	L	F	D	E
D	2				1		2	3		1						8	1			6	2	2		1	2	1	8	17
E	1	1					1		1	1	9		2			21	22			3	4	1	1	4			7	28
K	1		1		1			1		39	20		12	1		10	2		1	8	44		27	12	2	1	9	1
R		4		1	8			1	1	5	2		4	2	1	2				4	1		11	1	1		6	1
H					6			6	1																			
N	3	1	1					1	7		7	1	4			3	4			5		1						
Q		1		1	8	1				3	5		7			2	1	6		5	1	2	1	11			5	
S	3	7	12		17	7	2	33	8		3		13		39	5	1			8				8			1	4
T		2	2		2	45	1	1	1	5		8	5		5	2	3	3		3	2				1		3	1
G	5	15	21				2	4	37	1					2		1					3	1	6				
A	6		7		1	46					5				4		8	15		3		19	1	1			1	
P	5	4				1					1		1															
C	3			2	3			2				1	5							1		2						1
I		4	5		3	1					2	16		12			2	8				3			6	2		1
L	8	16				1		3			2	6		7	1		1	38	3			1			17	17		
V	2	1	4				1	1		1		23	2	33		1		4	1			14	7		7		2	1
M															4								4	7	6			
F	14		3	50								1	1	1			1	4	2				1	8	35			
W																								6				
Y	3			2	7																		1					

Consensus:

G F *x* T A S G K *o* *i* *x* *i* S *o* *o* S L *x* K A K *x* *i* F *o* D
S S S A V R *a* L E
N S

FIGURE 4

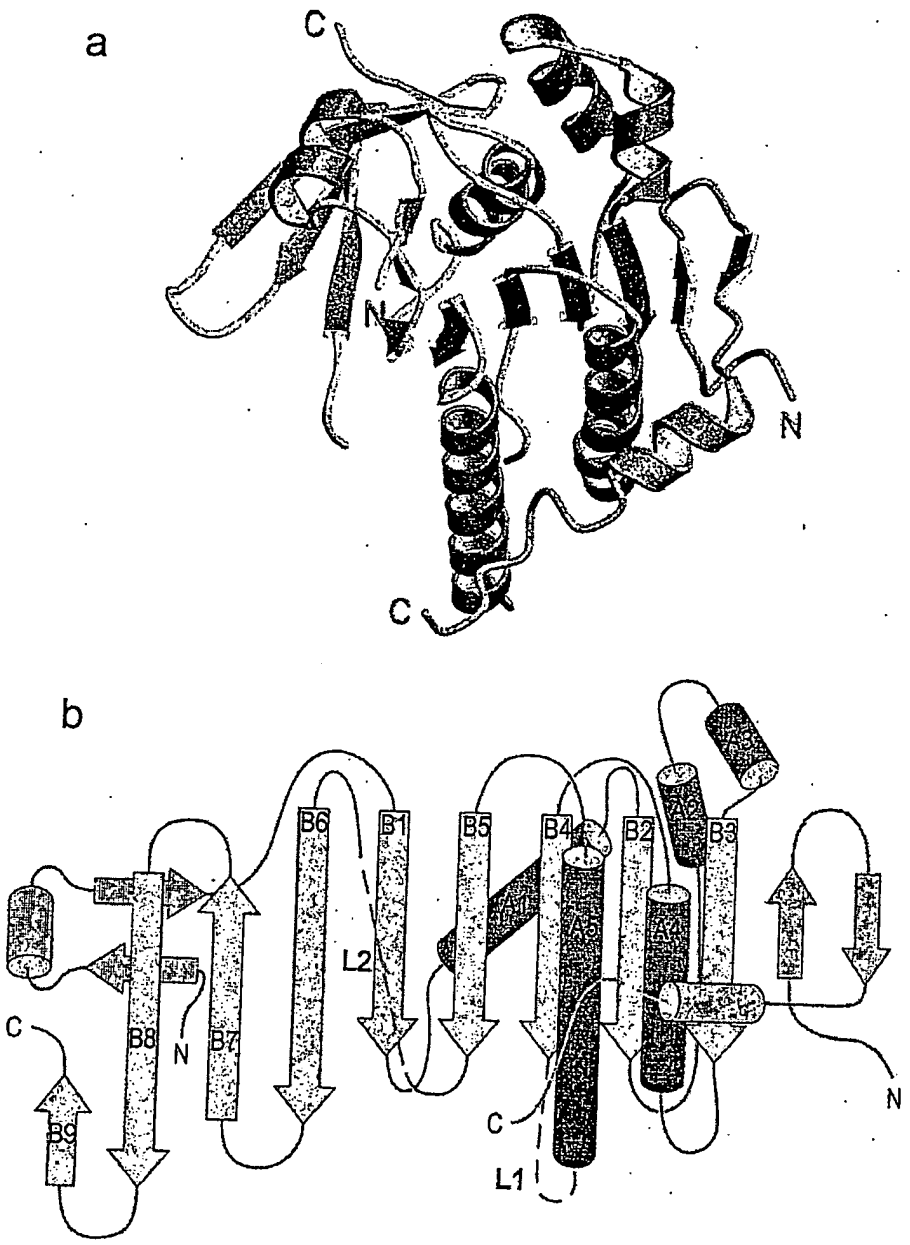


FIGURE 5

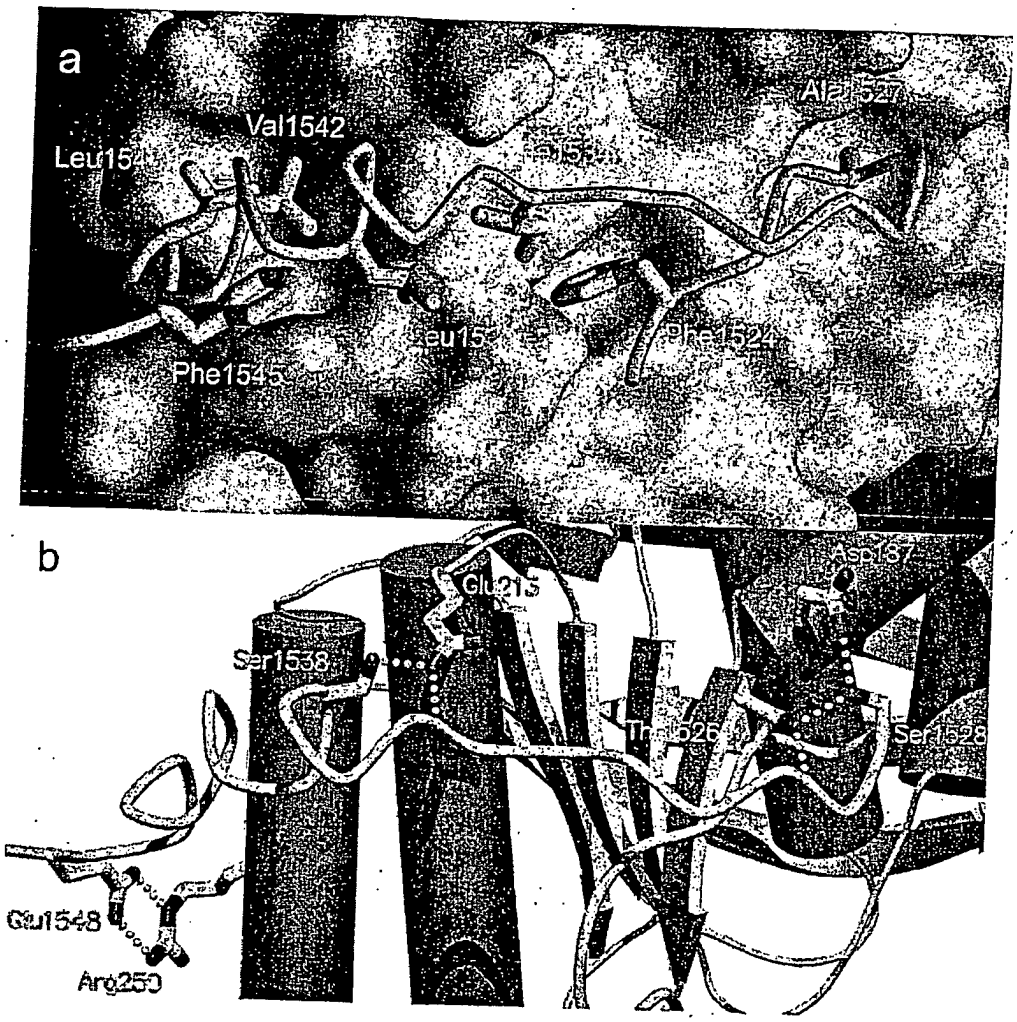

a
Val1542
Leu154
Phe1545
Phe1524
b
Glu213
Ser1538
Glu1548
Arg255

FIGURE 6

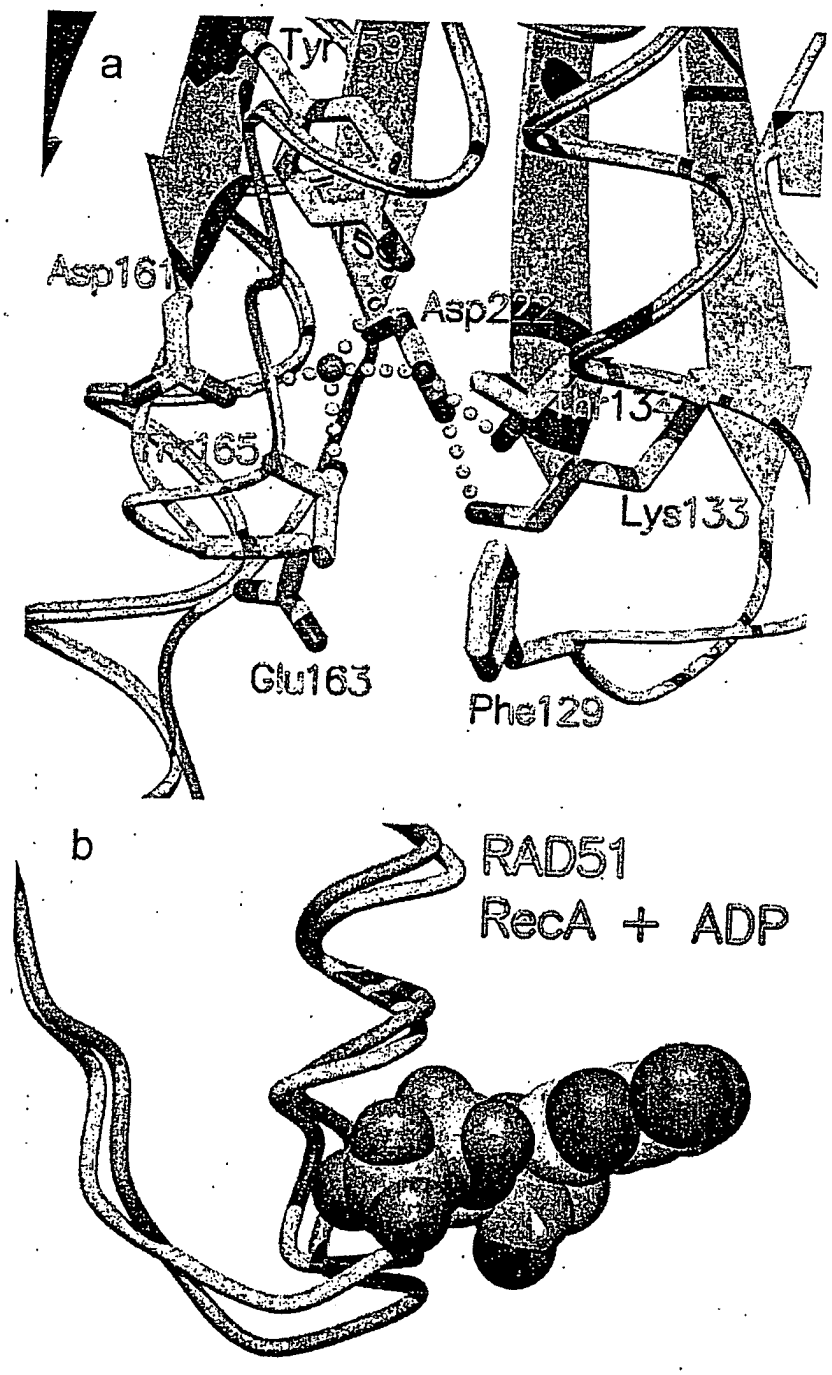
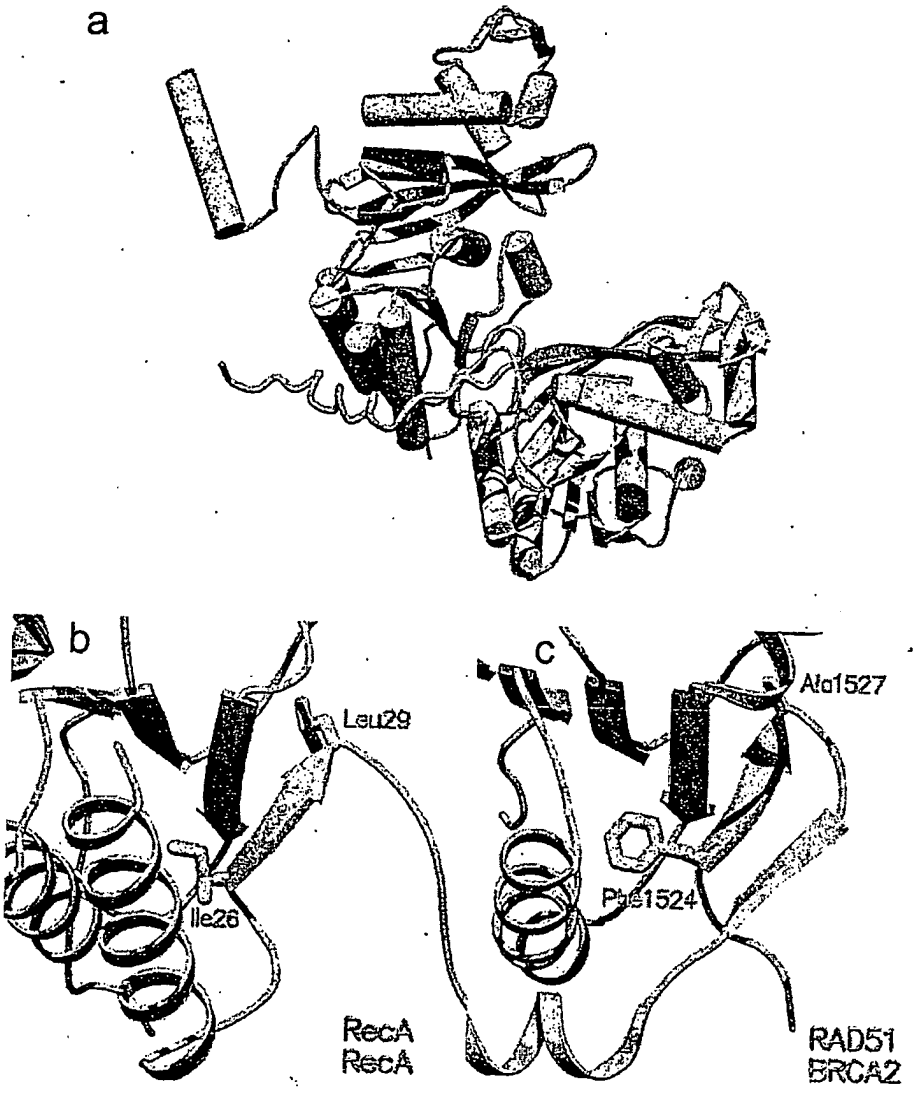

a
Tyr59
Asp161
Asp222
Arg165
Thr134
Lys133
Glu163
Phe129
b
RAD51
RecA + ADP

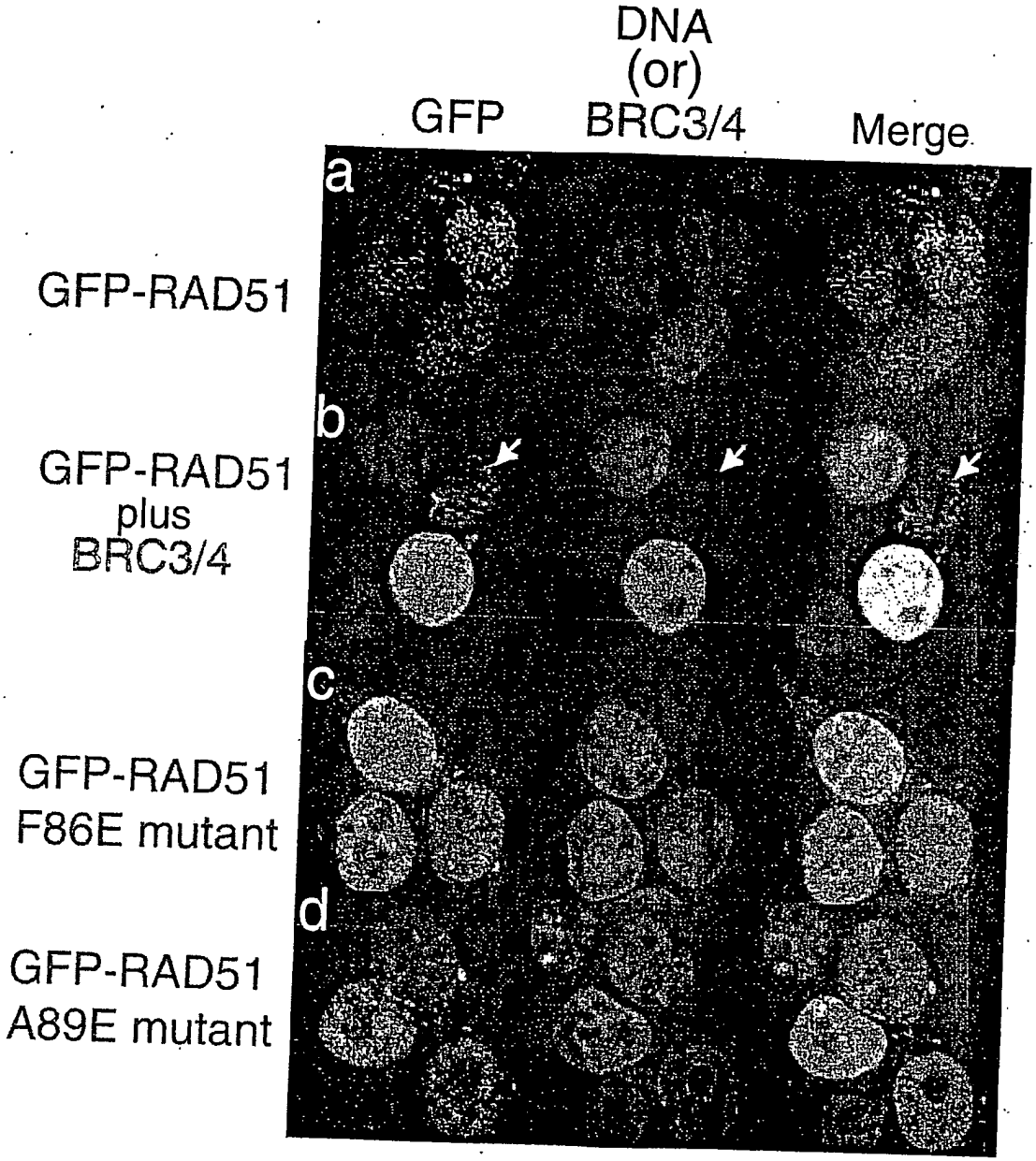
FIGURE 7



d

RAD51	H. sapiens	85-G	F T T A T E-91
"	C. griseus	85-G	F T T A T E-91
"	X. laevis	82-G	F T T A T E-88
"	D. melanogaster	82-G	F L S A R T-88
"	S. cerevisiae	143-G	F V T A A D-149
DMC1	H. sapiens	85-G	F L T A F E-91
RADA	P. furiosus	95-T	F M R A D E-102
RecA	E. coli	25-S	I M R L G E-31
BRCA2 BRC4	H. sapiens	1523-G	F H T A S G-1529

FIGURE 8


DNA
(or)
GFP
BRC3/4
Merge
a
b
c
d
GFP-RAD51
GFP-RAD51
plus
BRC3/4
GFP-RAD51
F86E mutant
GFP-RAD51
A89E mutant